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 <120> TITLE OF INVENTION: Novel TNF receptor death domain ligand proteins and inhibitors of ligand binding(as amended)
 <130> FILE REFERENCE: GFN-5232CP4DV3
 <140> CURRENT APPLICATION NUMBER: US/09/989,350
 <141> CURRENT FILING DATE: 2001-11-20
 <150> PRIOR APPLICATION NUMBER: 09/185,258
 <151> PRIOR FILING DATE: 1998-11-02
 <150> PRIOR APPLICATION NUMBER: 08/839,032
 <151> PRIOR FILING DATE: 1997-04-23
 <150> PRIOR APPLICATION NUMBER: 08/698,551
 <151> PRIOR FILING DATE: 1996-08-15
 <150> PRIOR APPLICATION NUMBER: 08/602,228
 <151> PRIOR FILING DATE: 1996-02-15
 <150> PRIOR APPLICATION NUMBER: 08/533,901
 <151> PRIOR FILING DATE: 1995-09-26
 <150> PRIOR APPLICATION NUMBER: 08/494,440
 <151> PRIOR FILING DATE: 1995-06-19
 <150> PRIOR APPLICATION NUMBER: 08/327,514
 <151> PRIOR FILING DATE: 1994-10-19
 <160> NUMBER OF SEQ ID NOS: 19
 <170> SOFTWARE: PatentIn Ver. 2.0

 <210> SEQ ID NO 1
 <211> LENGTH: 2158
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (2)..(1231)
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 Ser Asn Ala Gly Asp Gly Pro Gly Gly Glu Gly Ser Val His Leu Ala
 1 5 10 15
 agc tct cgg ggc act ttg tct gat agt gaa att gag acc aac tct gcc 97
 Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile Glu Thr Asn Ser Ala
 20 25 30
 aca agc acc atc ttt ggt aaa gcc cac agc ttg aag cca agc ata aag 145
 Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu Lys Pro Ser Ile Lys
 35 40 45
 gag aag ctg gca ggc agc ccc att cgt act tct gaa gat gtg agc cag 193
 Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser Glu Asp Val Ser Gln
 50 55 60
 cga gtc tat ctc tat gag gga ctc cta ggc aaa gag cgt tct act tta 241
 Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr Leu
 65 70 75 80
 tgg gac caa atg caa ttc tgg gaa gat gcc ttc tta gat gct gtg atg 289
 Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe Leu Asp Ala Val Met
 85 90 95
 ttg gag aga gaa ggg atg ggt atg gac cag ggt ccc cag gaa atg atc 337
 Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly Pro Gln Glu Met Ile
 100 105 110
 gac agg tac ctg tcc ctt gga gaa cat gac cgg aag cgc ctg gaa gat 385
 Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu Asp

	115		120		125											
gat	gaa	gat	cgc	ttg	ctg	gcc	aca	ctt	ctg	cac	aac	ctc	atc	tcc	tac	433
Asp	Glu	Asp	Arg	Leu	Leu	Ala	Thr	Leu	Leu	His	Asn	Leu	Ile	Ser	Tyr	
	130					135					140					
atg	ctg	ctg	atg	aag	gta	aat	aag	aat	gac	atc	cgc	aag	aag	gtg	agg	481
Met	Leu	Leu	Met	Lys	Val	Asn	Lys	Asn	Asp	Ile	Arg	Lys	Lys	Val	Arg	
	145				150					155				160		
cgc	cta	atg	gga	aag	tcg	cac	att	ggg	ctt	gtg	tac	agc	cag	caa	atc	529
Arg	Leu	Met	Gly	Lys	Ser	His	Ile	Gly	Leu	Val	Tyr	Ser	Gln	Gln	Ile	
				165					170					175		
aat	gag	gtg	ctt	gat	cag	ctg	gcg	aac	ctg	aat	gga	cgc	gat	ctc	tct	577
Asn	Glu	Val	Leu	Asp	Gln	Leu	Ala	Asn	Leu	Asn	Gly	Arg	Asp	Leu	Ser	
				180					185					190		
atc	tgg	tcc	agt	ggc	agc	cgg	cac	atg	aag	aag	cag	aca	ttt	gtg	gta	625
Ile	Trp	Ser	Ser	Gly	Ser	Arg	His	Met	Lys	Lys	Gln	Thr	Phe	Val	Val	
				195					200					205		
cat	gca	ggg	aca	gat	aca	aac	gga	gat	atc	ttt	ttc	atg	gag	gtg	tgc	673
His	Ala	Gly	Thr	Asp	Thr	Asn	Gly	Asp	Ile	Phe	Phe	Met	Glu	Val	Cys	
	210					215					220					
gat	gac	tgt	gtg	gtg	ttg	cgt	agt	aac	atc	gga	aca	gtg	tat	gag	cgc	721
Asp	Asp	Cys	Val	Val	Leu	Arg	Ser	Asn	Ile	Gly	Thr	Val	Tyr	Glu	Arg	
	225				230					235				240		
tgg	tgg	tac	gag	aag	ctc	atc	aac	atg	acc	tac	tgt	ccc	aag	acg	aag	769
Trp	Trp	Tyr	Glu	Lys	Leu	Ile	Asn	Met	Thr	Tyr	Cys	Pro	Lys	Thr	Lys	
				245					250					255		
gtg	ttg	tgc	ttg	tgg	cgt	aga	aat	ggc	tct	gag	acc	cag	ctc	aac	aag	817
Val	Leu	Cys	Leu	Trp	Arg	Arg	Asn	Gly	Ser	Glu	Thr	Gln	Leu	Asn	Lys	
				260				265						270		
ttc	tat	act	aaa	aag	tgt	cgg	gag	ctg	tac	tac	tgt	gtg	aag	gac	agc	865
Phe	Tyr	Thr	Lys	Lys	Cys	Arg	Glu	Leu	Tyr	Tyr	Cys	Val	Lys	Asp	Ser	
	275					280					285					
atg	gag	cgc	gct	gcc	gcc	cga	cag	caa	agc	atc	aaa	ccc	gga	cct	gaa	913
Met	Glu	Arg	Ala	Ala	Ala	Arg	Gln	Gln	Ser	Ile	Lys	Pro	Gly	Pro	Glu	
	290					295					300					
ttg	ggt	ggc	gag	ttc	cct	gtg	cag	gac	ctg	aag	act	ggt	gag	ggt	ggc	961
Leu	Gly	Gly	Glu	Phe	Pro	Val	Gln	Asp	Leu	Lys	Thr	Gly	Glu	Gly	Gly	
	305				310				315					320		
ctg	ctg	cag	gtg	acc	ctg	gaa	ggg	atc	aac	ctc	aaa	ttc	atg	cac	aat	1009
Leu	Leu	Gln	Val	Thr	Leu	Glu	Gly	Ile	Asn	Leu	Lys	Phe	Met	His	Asn	
				325					330					335		
cag	gtt	ttc	ata	gag	ctg	aat	cac	att	aaa	aag	tgc	aat	aca	gtt	cga	1057
Gln	Val	Phe	Ile	Glu	Leu	Asn	His	Ile	Lys	Lys	Cys	Asn	Thr	Val	Arg	
	340					345					350					
ggc	gtc	ttt	gtc	ctg	gag	gaa	ttt	gtt	cct	gaa	att	aaa	gaa	gtg	gtg	1105
Gly	Val	Phe	Val	Leu	Glu	Glu	Phe	Val	Pro	Glu	Ile	Lys	Glu	Val	Val	
	355					360					365					
agc	cac	aag	tac	aag	aca	cca	atg	gcc	cac	gaa	atc	tgc	tac	tcc	gta	1153
Ser	His	Lys	Tyr	Lys	Thr	Pro	Met	Ala	His	Glu	Ile	Cys	Tyr	Ser	Val	
	370					375					380					
tta	tgt	ctc	ttc	tcg	tac	gtg	gct	gca	gtt	cat	agc	agt	gag	gaa	gat	1201
Leu	Cys	Leu	Phe	Ser	Tyr	Val	Ala	Ala	Val	His	Ser	Ser	Glu	Glu	Asp	
	385				390					395				400		
ctc	aga	acc	ccg	ccc	cgg	cct	gtc	tct	agc	tgatggagag	gggctacgca					1251
Leu	Arg	Thr	Pro	Pro	Arg	Pro	Val	Ser	Ser							
				405					410							
gctgccccag	cccagggcac	gcccctggcc	ccttgctggt	cccaagtgca	cgatgctgct											1311
gtgactgagg	agtggatgat	gctcgtgtgt	cctctgcaag	ccccctgctg	tggtctgggt											1371

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gggtaccggt tatgtgtccc tctgagtgtg tcttgagcgt gtccaccttc tccctctcca 1431
ctcccagaag accaaactgc cttcccctca gggctcaaga atgtgtacag tctgtggggc 1491
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ccctggcggt aactgtccac tgcaagagtc tggctctccc ttctctgtga cccggcatga 1611
ctggg'gcgct ggagcagttt cactctgtga ggagtgaagg aaccctgggg ctcaccctct 1671
cagaggaagg gcacagagag gaagggaaga attggggggc agccggagtg agtggcagcc 1731
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gccttcggca tcagaggatg gagtggtcga ggctagtgga gtcccaggga ccgctggctg 1911
ctctgcctga gcatcaggga gggggcagga aagaccaagc tgggtttgca catctgtctg 1971
caggctgtct ctccaggcac ggggtgtcag gagggagaga cagcctgggt atgggcaaga 2031
aatgactgta aatatttcag cccacatta tttatagaaa atgtacagtt gtgtgaatgt 2091
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<210> SEQ ID NO 2

<211> LENGTH: 410

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

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Ser Asn Ala Gly Asp Gly Pro Gly Gly Glu Gly Ser Val His Leu Ala
 1             5             10             15
Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile Glu Thr Asn Ser Ala
 20             25             30
Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu Lys Pro Ser Ile Lys
 35             40             45
Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser Glu Asp Val Ser Gln
 50             55             60
Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys Glu Arg Ser Thr Leu
 65             70             75             80
Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe Leu Asp Ala Val Met
 85             90             95
Leu Glu Arg Glu Gly Met Gly Met Asp Gln Gly Pro Gln Glu Met Ile
100            105            110
Asp Arg Tyr Leu Ser Leu Gly Glu His Asp Arg Lys Arg Leu Glu Asp
115            120            125
Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser Tyr
130            135            140
Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val Arg
145            150            155            160
Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln Ile
165            170            175
Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu Ser
180            185            190
Ile Trp Ser Ser Gly Ser Arg His Met Lys Lys Gln Thr Phe Val Val
195            200            205
His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val Cys
210            215            220
Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu Arg
225            230            235            240
Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr Lys
245            250            255
Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn Lys
260            265            270
Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp Ser
275            280            285
Met Glu Arg Ala Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro Glu

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290	295	300
Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly Gly		
305	310	315
Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His Asn		320
	325	330
Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val Arg		335
	340	345
Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val Val		350
	355	360
Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser Val		365
	370	375
Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu Asp		380
385	390	395
Leu Arg Thr Pro Pro Arg Pro Val Ser Ser		400
	405	410

<210> SEQ ID NO 3

<211> LENGTH: 826

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (2)..(415)

<400> SEQUENCE: 3

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g gag gtg cag gac ctc ttc gaa gcc cag ggc aat gac cga ctg aag ctg 49
  Glu Val Gln Asp Leu Phe Glu Ala Gln Gly Asn Asp Arg Leu Lys Leu
    1           5           10          15
ctg gtg ctg tac agt gga gag gat gat gag ctg cta cag cgg gca gct 97
Leu Val Leu Tyr Ser Gly Glu Asp Asp Glu Leu Leu Gln Arg Ala Ala
    20          25          30
gcc ggg ggc ttg gcc atg ctt acc tcc atg cgg ccc acg ctc tgc agc 145
Ala Gly Gly Leu Ala Met Leu Thr Ser Met Arg Pro Thr Leu Cys Ser
    35          40          45
cgc att ccc caa gtg acc aca cac tgg ctg gag atc ctg cag gcc ctg 193
Arg Ile Pro Gln Val Thr Thr His Trp Leu Glu Ile Leu Gln Ala Leu
    50          55          60
ctt ctg agc tcc aac cag gag ctg cag cac cgg ggt gct gtg gtg gtg 241
Leu Leu Ser Ser Asn Gln Glu Leu Gln His Arg Gly Ala Val Val Val
    65          70          75          80
ctg aac atg gtg gag gcc tcg agg gag att gcc agc acc ctg atg gag 289
Leu Asn Met Val Glu Ala Ser Arg Glu Ile Ala Ser Thr Leu Met Glu
    85          90          95
agt gag atg atg gag atc ttg tca gtg cta gct aag ggt gac cac agc 337
Ser Glu Met Met Glu Ile Leu Ser Val Leu Ala Lys Gly Asp His Ser
   100         105         110
cct gtc aca agg gct gct gca gcc tgc ctg gac aaa gca gtg gaa tat 385
Pro Val Thr Arg Ala Ala Ala Cys Leu Asp Lys Ala Val Glu Tyr
   115         120         125
ggg ctt atc caa ccc aac caa gat gga gag tgaggggggtt gtccctgggc 435
Gly Leu Ile Gln Pro Asn Gln Asp Gly Glu
   130         135
ccaaggctca tgcacacgct acctattgtg gcacggagag taaggacgga agcagctttg 495
gctgggtggtg gctggcatgc ccaatactct tgcccatacct cgcttgctgc ctaggatgt 555
cctctgttct gagtcagcgg ccacgttcag tcacacagcc ctgcttgggc agcattgcct 615
gcagcctcac tcagagggggc cctttttctg tactactgta gtcagctggg aatggggaag 675
gtgcatccca acacagcctg tggatcctgg ggcatttgga agggcgacaca catcagcagc 735
ctcaccagct gtgagcctgc tatcaggcct gccctccaa taaaagtgtg tagaactcca 795

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a

826

<210> SEQ ID NO 4
 <211> LENGTH: 138
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 4

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Glu Val Gln Asp Leu Phe Glu Ala Gln Gly Asn Asp Arg Leu Lys Leu
 1           5           10           15
Leu Val Leu Tyr Ser Gly Glu Asp Asp Glu Leu Leu Gln Arg Ala Ala
 20           25           30
Ala Gly Gly Leu Ala Met Leu Thr Ser Met Arg Pro Thr Leu Cys Ser
 35           40           45
Arg Ile Pro Gln Val Thr Thr His Trp Leu Glu Ile Leu Gln Ala Leu
 50           55           60
Leu Leu Ser Ser Asn Gln Glu Leu Gln His Arg Gly Ala Val Val Val
 65           70           75           80
Leu Asn Met Val Glu Ala Ser Arg Glu Ile Ala Ser Thr Leu Met Glu
 85           90           95
Ser Glu Met Met Glu Ile Leu Ser Val Leu Ala Lys Gly Asp His Ser
100          105          110
Pro Val Thr Arg Ala Ala Ala Ala Cys Leu Asp Lys Ala Val Glu Tyr
115          120          125
Gly Leu Ile Gln Pro Asn Gln Asp Gly Glu
130          135
  
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<210> SEQ ID NO 5
 <211> LENGTH: 722
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (2)..(559)
 <400> SEQUENCE: 5

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g gag aag ccg ctg cac gcc ctg ctg cac ggc cgc ggg gtt tgc ctc aac 49
  Glu Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys Leu Asn
  1           5           10           15
gaa aag agc tac cgc gag caa gtc aag atc gag aga gac tcc cgt gag 97
  Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg Glu
  20           25           30
cac gag gag ccc acc acc tct gag atg gcc gag gag acc tac tcc ccc 145
  His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser Pro
  35           40           45
aag atc ttc cgg ccc aaa cac acc cgc atc tcc gag ctg aag gct gaa 193
  Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala Glu
  50           55           60
gca gtg aag aag gac cgc aga aag aag ctg acc cag tcc aag ttt gtc 241
  Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe Val
  65           70           75           80
ggg gga gcc gag aac act gcc cac ccc cgg atc atc tct gaa cct gag 289
  Gly Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Glu Pro Glu
  85           90           95
atg aga cag gag tct gag cag ggc ccc tgc cgc aga cac atg gag gct 337
  Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu Ala
  100          105          110
tcc ctg cag gag ctc aaa gcc agc cca cgc atg gtg ccc cgt gct gtg 385
  Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg Ala Val
  
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      115              120              125
tac ctg ccc aat tgt gac cgc aaa gga ttc tac aag aga aag cag tgc 433
Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln Cys
      130              135              140
aaa cct tcc cgt ggc cgc aag cgt ggc atc tgc tgg tgc gtg gac aag 481
Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp Lys
      145              150              155              160
tac ggg atg aag ctg cca ggc atg gag tac gtt gac ggg gac ttt cag 529
Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe Gln
      165              170              175
tgc cac acc ttc gac agc agc aac gtt gag tgatgcgtcc ccccccaacc 579
Cys His Thr Phe Asp Ser Ser Asn Val Glu
      180              185
tttccctcac ccccttcac cccagcccc gactccagcc agcgcctccc tccaccccag 639
gacgccactc atttcattctc atttaaggga aaaatatata tctatctatt tgaggaaaaa 699
aaaaaaaaaa aaaaaaaaaa aaa 722

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<210> SEQ ID NO 6

<211> LENGTH: 186

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

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Glu Lys Pro Leu His Ala Leu Leu His Gly Arg Gly Val Cys Leu Asn
 1              5              10              15
Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu Arg Asp Ser Arg Glu
      20              25              30
His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser Pro
      35              40              45
Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala Glu
      50              55              60
Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe Val
      65              70              75              80
Gly Gly Ala Glu Asn Thr Ala His Pro Arg Ile Ile Ser Glu Pro Glu
      85              90              95
Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu Ala
      100              105              110
Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met Val Pro Arg Ala Val
      115              120              125
Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln Cys
      130              135              140
Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp Lys
      145              150              155              160
Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe Gln
      165              170              175
Cys His Thr Phe Asp Ser Ser Asn Val Glu
      180              185

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<210> SEQ ID NO 7

<211> LENGTH: 1023

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (57)..(872)

<400> SEQUENCE: 7

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ccctgcactc tcgtctctct gccccacccc gaggtaaagg gggcgactaa gagaag atg 59
Met

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1

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gtg ttg ctc acc gcg gtc ctc ctg ctg ctg gcc gcc tat gcg ggg ccg 107
Val Leu Leu Thr Ala Val Leu Leu Leu Leu Ala Ala Tyr Ala Gly Pro
      5      10      15
gcc cag agc ctg ggc tcc ttc gtg cac tgc gag ccc tgc gac gag aaa 155
Ala Gln Ser Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu Lys
      20      25      30
gcc ctc tcc atg tgc ccc ccc agc ccc ctg ggc tgc gag ctg gtc aag 203
Ala Leu Ser Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val Lys
      35      40      45
gag ccg ggc tgc ggc tgc tgc atg acc tgc gcc ctg gcc gag ggg cag 251
Glu Pro Gly Cys Gly Cys Cys Met Thr Cys Ala Leu Ala Glu Gly Gln
      50      55      60      65
tcg tgc ggc gtc tac acc gag cgc tgc gcc cag ggg ctg cgc tgc ctc 299
Ser Cys Gly Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys Leu
      70      75      80
ccc cgg cag gac gag gag aag ccg ctg cac gcc ctg ctg cac ggc cgc 347
Pro Arg Gln Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly Arg
      85      90      95
ggg gtt tgc ctc aac gaa aag agc tac cgc gag caa gtc aag atc gag 395
Gly Val Cys Leu Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile Glu
      100      105      110
aga gac tcc cgt gag cac gag gag ccc acc acc tct gag atg gcc gag 443
Arg Asp Ser Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu
      115      120      125
gag acc tac tcc ccc aag atc ttc cgg ccc aaa cac acc cgc atc tcc 491
Glu Thr Tyr Ser Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile Ser
      130      135      140      145
gag ctg aag gct gaa gca gtg aag aag gac cgc aga aag aag ctg acc 539
Glu Leu Lys Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr
      150      155      160
cag tcc aag ttt gtc ggg gga gcc gag aac act gcc cac ccc cgg atc 587
Gln Ser Lys Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg Ile
      165      170      175
atc tct gca cct gag atg aga cag gag tct gag cag ggc ccc tgc cgc 635
Ile Ser Ala Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg
      180      185      190
aga cac atg gag gct tcc ctg cag gag ctc aaa gcc agc cca cgc atg 683
Arg His Met Glu Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg Met
      195      200      205
gtg ccc cgt gct gtg tac ctg ccc aat tgt gac cgc aaa gga ttc tac 731
Val Pro Arg Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr
      210      215      220      225
aag aga aag cag tgc aaa cct tcc cgt ggc cgc aag cgt ggc atc tgc 779
Lys Arg Lys Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys
      230      235      240
tgg tgc gtg gac aag tac ggg atg aag ctg cca ggc atg gag tac gtt 827
Trp Cys Val Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val
      245      250      255
gac ggg gac ttt cag tgc cac acc ttc gac agc agc aac gtt gag 872
Asp Gly Asp Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu
      260      265      270
tgatgcgtcc ccccccaacc ttccctcac ccctccac cccagcccc gactccagcc 932
agcgccctccc tccaccccag gacgccactc atttcactc atttaaggga aaaatatata 992
tctatctatt tgaaaaaaaaa aaaaaaaacc c 1023

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<210> SEQ ID NO 8

<211> LENGTH: 272

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

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Met Val Leu Leu Thr Ala Val Leu Leu Leu Leu Ala Ala Tyr Ala Gly
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Pro Ala Gln Ser Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu
          20           25           30
Lys Ala Leu Ser Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val
          35           40           45
Lys Glu Pro Gly Cys Gly Cys Cys Met Thr Cys Ala Leu Ala Glu Gly
          50           55           60
Gln Ser Cys Gly Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys
          65           70           75           80
Leu Pro Arg Gln Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly
          85           90           95
Arg Gly Val Cys Leu Asn Glu Lys Ser Tyr Arg Glu Gln Val Lys Ile
          100          105          110
Glu Arg Asp Ser Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala
          115          120          125
Glu Glu Thr Tyr Ser Pro Lys Ile Phe Arg Pro Lys His Thr Arg Ile
          130          135          140
Ser Glu Leu Lys Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu
          145          150          155          160
Thr Gln Ser Lys Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg
          165          170          175
Ile Ile Ser Ala Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys
          180          185          190
Arg Arg His Met Glu Ala Ser Leu Gln Glu Leu Lys Ala Ser Pro Arg
          195          200          205
Met Val Pro Arg Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe
          210          215          220
Tyr Lys Arg Lys Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile
          225          230          235          240
Cys Trp Cys Val Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr
          245          250          255
Val Asp Gly Asp Phe Gln Cys His Thr Phe Asp Ser Ser Asn Val Glu
          260          265          270
```

<210> SEQ ID NO 9

<211> LENGTH: 1694

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (2)..(931)

<400> SEQUENCE: 9

```
c tct ctc aag gcc aac atc cct gag gtg gaa gct gtc ctc aac acc gac 49
  Ser Leu Lys Ala Asn Ile Pro Glu Val Glu Ala Val Leu Asn Thr Asp
  1           5           10           15
agg agt ttg gtg tgt gat ggg aag agg ggc tta tta act cgt ctg ctg 97
Arg Ser Leu Val Cys Asp Gly Lys Arg Gly Leu Leu Thr Arg Leu Leu
          20           25           30
cag gtc atg aag aag gag cca gca gag tcg tct ttc agg ttt tgg caa 145
Gln Val Met Lys Lys Glu Pro Ala Glu Ser Ser Phe Arg Phe Trp Gln
          35           40           45
gct cgg gct gtg gag agt ttc ctc cga ggg acc acc tcc tat gca gac 193
```


Ala	Arg	Ala	Val	Glu	Ser	Phe	Leu	Arg	Gly	Thr	Thr	Ser	Tyr	Ala	Asp	
50						55					60					
cag	atg	ttc	ctg	ctg	aag	cga	ggc	ctc	ttg	gag	cac	atc	ctt	tac	tgc	241
Gln	Met	Phe	Leu	Leu	Lys	Arg	Gly	Leu	Leu	Glu	His	Ile	Leu	Tyr	Cys	
65					70					75					80	
att	gtg	gac	agc	gag	tgt	aag	tca	agg	gat	gtg	ctc	cag	agt	tac	ttt	289
Ile	Val	Asp	Ser	Glu	Cys	Lys	Ser	Arg	Asp	Val	Leu	Gln	Ser	Tyr	Phe	
				85					90					95		
gac	ctc	ctg	ggg	gag	ctg	atg	aag	ttc	aac	gtt	gat	gca	ttc	aag	aga	337
Asp	Leu	Leu	Gly	Glu	Leu	Met	Lys	Phe	Asn	Val	Asp	Ala	Phe	Lys	Arg	
			100					105					110			
ttc	aat	aaa	tat	atc	aac	acc	gat	gca	aag	ttc	cag	gta	ttc	ctg	aag	385
Phe	Asn	Lys	Tyr	Ile	Asn	Thr	Asp	Ala	Lys	Phe	Gln	Val	Phe	Leu	Lys	
		115					120					125				
cag	atc	aac	agc	tcc	ctg	gtg	gac	tcc	aac	atg	ctg	gtg	cgc	tgt	gtc	433
Gln	Ile	Asn	Ser	Ser	Leu	Val	Asp	Ser	Asn	Met	Leu	Val	Arg	Cys	Val	
	130					135						140				
act	ctg	tcc	ctg	gac	cga	ttt	gaa	aac	cag	gtg	gat	atg	aaa	gtt	gcc	481
Thr	Leu	Ser	Leu	Asp	Arg	Phe	Glu	Asn	Gln	Val	Asp	Met	Lys	Val	Ala	
	145				150					155					160	
gag	gta	ctg	tct	gaa	tgc	cgc	ctg	ctc	gcc	tac	ata	tcc	cag	gtg	ccc	529
Glu	Val	Leu	Ser	Glu	Cys	Arg	Leu	Leu	Ala	Tyr	Ile	Ser	Gln	Val	Pro	
				165					170					175		
acg	cag	atg	tcc	ttc	ctc	ttc	cgc	ctc	atc	aac	atc	atc	cac	gtg	cag	577
Thr	Gln	Met	Ser	Phe	Leu	Phe	Arg	Leu	Ile	Asn	Ile	Ile	His	Val	Gln	
			180					185					190			
acg	ctg	acc	cag	gag	aac	gtc	agc	tgc	ctc	aac	acc	agc	ctg	gtg	atc	625
Thr	Leu	Thr	Gln	Glu	Asn	Val	Ser	Cys	Leu	Asn	Thr	Ser	Leu	Val	Ile	
		195					200					205				
ctg	atg	ctg	gcc	cga	cgg	aaa	gag	cgg	ctg	ccc	ctg	tac	ctg	cgg	ctg	673
Leu	Met	Leu	Ala	Arg	Arg	Lys	Glu	Arg	Leu	Pro	Leu	Tyr	Leu	Arg	Leu	
	210					215						220				
ctg	cag	cgg	atg	gag	cac	agc	aag	aag	tac	ccc	ggc	ttc	ctg	ctc	aac	721
Leu	Gln	Arg	Met	Glu	His	Ser	Lys	Lys	Tyr	Pro	Gly	Phe	Leu	Leu	Asn	
	225				230					235					240	
aac	ttc	cac	aac	ctg	ctg	cgc	ttc	tgg	cag	cag	cac	tac	ctg	cac	aag	769
Asn	Phe	His	Asn	Leu	Leu	Arg	Phe	Trp	Gln	Gln	His	Tyr	Leu	His	Lys	
			245						250					255		
gac	aag	gac	agc	acc	tgc	cta	gag	aac	agc	tcc	tgc	atc	agc	ttc	tca	817
Asp	Lys	Asp	Ser	Thr	Cys	Leu	Glu	Asn	Ser	Ser	Cys	Ile	Ser	Phe	Ser	
			260					265					270			
tac	tgg	aag	gag	aca	gtg	tcc	atc	ctg	ttg	aac	ccg	gac	cgg	cag	tca	865
Tyr	Trp	Lys	Glu	Thr	Val	Ser	Ile	Leu	Leu	Asn	Pro	Asp	Arg	Gln	Ser	
		275					280						285			
ccc	tct	gct	ctc	gtt	agc	tac	att	gag	gag	ccc	tac	atg	gac	ata	gac	913
Pro	Ser	Ala	Leu	Val	Ser	Tyr	Ile	Glu	Glu	Pro	Tyr	Met	Asp	Ile	Asp	
	290					295					300					
agg	gac	ttc	act	gag	gag	tgac	cttggg	ccagg	cctcg	ggagg	ctgct					961
Arg	Asp	Phe	Thr	Glu	Glu											
	305				310											
ggg	ccagtgt	gggtgagcgt	gggtacgatg	ccacacgccc	tgccctgttc	ccgttctctcc	1021									
ctg	ctgctctct	ctgcctgccc	caggtcctttg	ggtacaggct	tggtgggagg	gaagtcctag	1081									
aag	cccttg	tccccctggg	tctgagggcc	ctaggtcatg	gagagcctca	gtccccataa	1141									
tgagg	acagg	gtaccatgcc	cacctttcct	tcagaacct	ggggccagg	gccaccaga	1201									
ggta	agagga	catttagcat	tagctctgtg	tgagctcctg	ccggtttctt	ggctgtcagt	1261									
cagt	ccaga	gtggggagga	agatatgggt	gacccccacc	ccccatctgt	gagccaagcc	1321									
tcc	ttgtcc	ctggcctttg	gaccaggca	aaggcttctg	agccctgggc	aggggtggtg	1381									

```

ggtaccagag aatgctgcct tcccccaagc ctgcccctct gcctcatttt cctgtagctc 1441
ctctggttct gtttgctcat tggccgctgt gttcatccaa gggggttctc ccagaagtga 1501
ggggcctttc cctccatccc ttggggcacg gggcagctgt gcctgccctg cctctgcctg 1561
aggcagccgc tctgcctga gcctggacat ggggcccttc cttgtgttgc caatttatta 1621
acagcaaata aaccaattaa atggagacta ttaaataact ttattttaaa aatgaaaaaa 1681
aaaaaaaaa aaa 1694

```

<210> SEQ ID NO 10
 <211> LENGTH: 310
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 10

```

Ser Leu Lys Ala Asn Ile Pro Glu Val Glu Ala Val Leu Asn Thr Asp
 1             5             10             15
Arg Ser Leu Val Cys Asp Gly Lys Arg Gly Leu Leu Thr Arg Leu Leu
 20             25             30
Gln Val Met Lys Lys Glu Pro Ala Glu Ser Ser Phe Arg Phe Trp Gln
 35             40             45
Ala Arg Ala Val Glu Ser Phe Leu Arg Gly Thr Thr Ser Tyr Ala Asp
 50             55             60
Gln Met Phe Leu Leu Lys Arg Gly Leu Leu Glu His Ile Leu Tyr Cys
 65             70             75             80
Ile Val Asp Ser Glu Cys Lys Ser Arg Asp Val Leu Gln Ser Tyr Phe
 85             90             95
Asp Leu Leu Gly Glu Leu Met Lys Phe Asn Val Asp Ala Phe Lys Arg
100            105            110
Phe Asn Lys Tyr Ile Asn Thr Asp Ala Lys Phe Gln Val Phe Leu Lys
115            120            125
Gln Ile Asn Ser Ser Leu Val Asp Ser Asn Met Leu Val Arg Cys Val
130            135            140
Thr Leu Ser Leu Asp Arg Phe Glu Asn Gln Val Asp Met Lys Val Ala
145            150            155            160
Glu Val Leu Ser Glu Cys Arg Leu Leu Ala Tyr Ile Ser Gln Val Pro
165            170            175
Thr Gln Met Ser Phe Leu Phe Arg Leu Ile Asn Ile Ile His Val Gln
180            185            190
Thr Leu Thr Gln Glu Asn Val Ser Cys Leu Asn Thr Ser Leu Val Ile
195            200            205
Leu Met Leu Ala Arg Arg Lys Glu Arg Leu Pro Leu Tyr Leu Arg Leu
210            215            220
Leu Gln Arg Met Glu His Ser Lys Lys Tyr Pro Gly Phe Leu Leu Asn
225            230            235            240
Asn Phe His Asn Leu Leu Arg Phe Trp Gln Gln His Tyr Leu His Lys
245            250            255
Asp Lys Asp Ser Thr Cys Leu Glu Asn Ser Ser Cys Ile Ser Phe Ser
260            265            270
Tyr Trp Lys Glu Thr Val Ser Ile Leu Leu Asn Pro Asp Arg Gln Ser
275            280            285
Pro Ser Ala Leu Val Ser Tyr Ile Glu Glu Pro Tyr Met Asp Ile Asp
290            295            300
Arg Asp Phe Thr Glu Glu
305            310

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<210> SEQ ID NO 11
 <211> LENGTH: 2735
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (2)..(1822)

<400> SEQUENCE: 11

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g gag atc agt cgg aag gtg tac aag gga atg tta gac ctc ctc aag tgt 49
  Glu Ile Ser Arg Lys Val Tyr Lys Gly Met Leu Asp Leu Leu Lys Cys
    1           5           10          15
aca gtc ctc agc ttg gag cag tcc tat gcc cac gcg ggt ctg ggt ggc 97
Thr Val Leu Ser Leu Glu Gln Ser Tyr Ala His Ala Gly Leu Gly Gly
          20          25          30
atg gcc agc atc ttt ggg ctt ttg gag att gcc cag acc cac tac tat 145
Met Ala Ser Ile Phe Gly Leu Leu Glu Ile Ala Gln Thr His Tyr Tyr
          35          40          45
agt aaa gaa cca gac aag cgg aag aga agt cca aca gaa agt gta aat 193
Ser Lys Glu Pro Asp Lys Arg Lys Arg Ser Pro Thr Glu Ser Val Asn
          50          55          60
acc cca gtt ggc aag gat cct ggc cta gct ggg cgg ggg gac cca aag 241
Thr Pro Val Gly Lys Asp Pro Gly Leu Ala Gly Arg Gly Asp Pro Lys
          65          70          75          80
gct atg gca caa ctg aga gtt cca caa ctg gga cct cgg gca cca agt 289
Ala Met Ala Gln Leu Arg Val Pro Gln Leu Gly Pro Arg Ala Pro Ser
          85          90          95
gcc aca gga aag ggt cct aag gaa ctg gac acc aga agt tta aag gaa 337
Ala Thr Gly Lys Gly Pro Lys Glu Leu Asp Thr Arg Ser Leu Lys Glu
          100          105          110
gaa aat ttt ata gca tct att ggg cct gaa gta atc aaa cct gtc ttt 385
Glu Asn Phe Ile Ala Ser Ile Gly Pro Glu Val Ile Lys Pro Val Phe
          115          120          125
gac ctt ggt gag aca gag gag aaa aag tcc cag atc agc gca gac agt 433
Asp Leu Gly Glu Thr Glu Glu Lys Lys Ser Gln Ile Ser Ala Asp Ser
          130          135          140
ggt gtg agc ctg acg tct agt tcc cag agg act gat caa gac tct gtc 481
Gly Val Ser Leu Thr Ser Ser Ser Gln Arg Thr Asp Gln Asp Ser Val
          145          150          155          160
atc ggc gtg agt cca gct gtt atg atc cgc agc tca agt cag gat tct 529
Ile Gly Val Ser Pro Ala Val Met Ile Arg Ser Ser Ser Gln Asp Ser
          165          170          175
gaa gtt agc acc gtg gtg agt aat agc tct gga gag acc ctt gga gct 577
Glu Val Ser Thr Val Val Ser Asn Ser Ser Gly Glu Thr Leu Gly Ala
          180          185          190
gac agt gac ttg agc agc aat gca ggt gat gga cca ggt ggc gag ggc 625
Asp Ser Asp Leu Ser Ser Asn Ala Gly Asp Gly Pro Gly Gly Glu Gly
          195          200          205
agt gtt cac ctg gca agc tct cgg ggc act ttg tct gat agt gaa att 673
Ser Val His Leu Ala Ser Ser Arg Gly Thr Leu Ser Asp Ser Glu Ile
          210          215          220
gag acc aac tct gcc aca agc acc atc ttt ggt aaa gcc cac agc ttg 721
Glu Thr Asn Ser Ala Thr Ser Thr Ile Phe Gly Lys Ala His Ser Leu
          225          230          235          240
aag cca agc ata aag gag aag ctg gca ggc agc ccc att cgt act tct 769
Lys Pro Ser Ile Lys Glu Lys Leu Ala Gly Ser Pro Ile Arg Thr Ser
          245          250          255
gaa gat gtg agc cag cga gtc tat ctc tat gag gga ctc cta ggc aaa 817
Glu Asp Val Ser Gln Arg Val Tyr Leu Tyr Glu Gly Leu Leu Gly Lys
          260          265          270
gag cgt tct act tta tgg gac caa atg caa ttc tgg gaa gat gcc ttc 865
Glu Arg Ser Thr Leu Trp Asp Gln Met Gln Phe Trp Glu Asp Ala Phe
```

	275		280		285		
tta	gat	gct	gtg	atg	ttg	gag	aga
Leu	Asp	Ala	Val	Met	Leu	Glu	Arg
	290		295		300		
ccc	cag	gaa	atg	atc	gac	agg	tac
Pro	Gln	Glu	Met	Ile	Asp	Arg	Tyr
	305		310		315		320
aag	cgc	ctg	gaa	gat	gat	gaa	gat
Lys	Arg	Leu	Glu	Asp	Asp	Glu	Asp
			325			330	335
aac	ctc	atc	tcc	tac	atg	ctg	ctg
Asn	Leu	Ile	Ser	Tyr	Met	Leu	Leu
			340			345	350
cgc	aag	aag	gtg	agg	cgc	cta	atg
Arg	Lys	Lys	Val	Arg	Arg	Leu	Met
			355			360	365
tac	agc	cag	caa	atc	aat	gag	gtg
Tyr	Ser	Gln	Gln	Ile	Asn	Glu	Val
			370			375	380
gga	cgc	gat	ctc	tct	atc	tgg	tcc
Gly	Arg	Asp	Leu	Ser	Ile	Trp	Ser
			385			390	395
cag	aca	ttt	gtg	gta	cat	gca	ggg
Gln	Thr	Phe	Val	Val	His	Ala	Gly
			405			410	415
ttc	atg	gag	gtg	tgc	gat	gac	tgt
Phe	Met	Glu	Val	Cys	Asp	Asp	Cys
			420			425	430
aca	gtg	tat	gag	cgc	tgg	tgg	tac
Thr	Val	Tyr	Glu	Arg	Trp	Trp	Tyr
			435			440	445
tgt	ccc	aag	acg	aag	gtg	ttg	tgc
Cys	Pro	Lys	Thr	Lys	Val	Leu	Cys
			450			455	460
acc	cag	ctc	aac	aag	ttc	tat	act
Thr	Gln	Leu	Asn	Lys	Phe	Tyr	Thr
			465			470	475
tgt	gtg	aag	gac	agc	atg	gag	cgc
Cys	Val	Lys	Asp	Ser	Met	Glu	Arg
			485			490	495
aaa	ccc	gga	cct	gaa	ttg	ggt	ggc
Lys	Pro	Gly	Pro	Glu	Leu	Gly	Gly
			500			505	510
act	ggt	gag	ggt	ggc	ctg	ctg	cag
Thr	Gly	Glu	Gly	Gly	Leu	Leu	Gln
			515			520	525
aaa	ttc	atg	cac	aat	cag	ggt	ttc
Lys	Phe	Met	His	Asn	Gln	Val	Phe
			530			535	540
tgc	aat	aca	gtt	cga	ggc	gtc	ttt
Cys	Asn	Thr	Val	Arg	Gly	Val	Phe
			545			550	555
att	aaa	gaa	gtg	gtg	agc	cac	aag
Ile	Lys	Glu	Val	Val	Ser	His	Lys
			565			570	575
atc	tgc	tac	tcc	gta	tta	tgt	ctc
Ile	Cys	Tyr	Ser	Val	Leu	Cys	Leu

580	585	590	
agc agt gag gaa gat ctc aga acc ccg ccc cgg cct gtc tct agc			1822
Ser Ser Glu Glu Asp Leu Arg Thr Pro Pro Arg Pro Val Ser Ser			
595	600	605	
tgatggagag gggctacgca gctgccccag cccagggcac gcccttggtt			1882
cccaagtgcg cgatgctgct gtgactgagg agtggatgat gctcgtgtgt cctctgcaag			1942
ccccctgctg tggcttggtt gggtaccggt tatgtgtccc tctgagtgtg tcttgagcgt			2002
gtccaccttc tccctctcca ctcccagaag accaaaactgc cttccccctca gggctcaaga			2062
atgtgtacag tctgtggggc cgggtgtgaac ccactatttt gtgtccttga gacatttgtg			2122
ttgtggttcc ttgtccttgt ccctggcggt ataactgtcc actgcaagag tctggctctc			2182
ccttctctgt gacccggcat gactgggcgc ctggagcagt ttcactctgt gaggagttag			2242
ggaaccctgg ggctcaccct ctcagaggaa gggcacagag aggaagggaa gaattggggg			2302
gcagccggag tgagtggcag cctccctgct tccttctgca ttcccaagcc ggcagctact			2362
gcccagggcc cgcagtgtg gctgctgcct gccacagcct ctgtgactgc agtggagcgg			2422
cgaattccct gtggcctgcc acgccttcgg catcagagga tggagtggc gaggctagt			2482
gagtcccagg gaccgctggc tgctctgcct gagcatcagg gagggggcag gaaagaccaa			2542
gctgggtttg cacatctgtc tgcaggctgt ctctccaggc acgggggtgtc agggaggaga			2602
gacagcctgg gtatgggcaa gaaatgactg taaatatttc agccccacat tatttataga			2662
aaatgtacag ttgtgtgaat gtgaaataaa tgtcctcaac tccccaaaaa aaaaaaaaaa			2722
aaaaaaaaaa aaa			2735

<210> SEQ ID NO 12

<211> LENGTH: 607

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Glu	Ile	Ser	Arg	Lys	Val	Tyr	Lys	Gly	Met	Leu	Asp	Leu	Leu	Lys	Cys
1				5					10					15	
Thr	Val	Leu	Ser	Leu	Glu	Gln	Ser	Tyr	Ala	His	Ala	Gly	Leu	Gly	Gly
		20						25					30		
Met	Ala	Ser	Ile	Phe	Gly	Leu	Leu	Glu	Ile	Ala	Gln	Thr	His	Tyr	Tyr
		35					40					45			
Ser	Lys	Glu	Pro	Asp	Lys	Arg	Lys	Arg	Ser	Pro	Thr	Glu	Ser	Val	Asn
	50					55					60				
Thr	Pro	Val	Gly	Lys	Asp	Pro	Gly	Leu	Ala	Gly	Arg	Gly	Asp	Pro	Lys
	65				70					75					80
Ala	Met	Ala	Gln	Leu	Arg	Val	Pro	Gln	Leu	Gly	Pro	Arg	Ala	Pro	Ser
			85						90					95	
Ala	Thr	Gly	Lys	Gly	Pro	Lys	Glu	Leu	Asp	Thr	Arg	Ser	Leu	Lys	Glu
			100					105					110		
Glu	Asn	Phe	Ile	Ala	Ser	Ile	Gly	Pro	Glu	Val	Ile	Lys	Pro	Val	Phe
		115					120					125			
Asp	Leu	Gly	Glu	Thr	Glu	Glu	Lys	Lys	Ser	Gln	Ile	Ser	Ala	Asp	Ser
	130					135					140				
Gly	Val	Ser	Leu	Thr	Ser	Ser	Ser	Gln	Arg	Thr	Asp	Gln	Asp	Ser	Val
	145				150					155				160	
Ile	Gly	Val	Ser	Pro	Ala	Val	Met	Ile	Arg	Ser	Ser	Ser	Gln	Asp	Ser
			165						170					175	
Glu	Val	Ser	Thr	Val	Val	Ser	Asn	Ser	Ser	Gly	Glu	Thr	Leu	Gly	Ala
		180						185					190		
Asp	Ser	Asp	Leu	Ser	Ser	Asn	Ala	Gly	Asp	Gly	Pro	Gly	Gly	Glu	Gly
		195					200					205			
Ser	Val	His	Leu	Ala	Ser	Ser	Arg	Gly	Thr	Leu	Ser	Asp	Ser	Glu	Ile
	210					215					220				
Glu	Thr	Asn	Ser	Ala	Thr	Ser	Thr	Ile	Phe	Gly	Lys	Ala	His	Ser	Leu
	225				230					235					240
Lys	Pro	Ser	Ile	Lys	Glu	Lys	Leu	Ala	Gly	Ser	Pro	Ile	Arg	Thr	Ser

acc ctc tcc gcg atg act gcc agc tca gtg gag cag ctg cgg aag gag	95
Thr Leu Ser Ala Met Thr Ala Ser Ser Val Glu Gln Leu Arg Lys Glu	
20 25 30	
ggc aat gag ctg ttc aaa tgt gga gac tac ggg ggc gcc ctg gcg gcc	143
Gly Asn Glu Leu Phe Lys Cys Gly Asp Tyr Gly Gly Ala Leu Ala Ala	
35 40 45	
tac act cag gcc ctg ggt ctg gac gcg acg ccc cag gac cag gcc gtt	191
Tyr Thr Gln Ala Leu Gly Leu Asp Ala Thr Pro Gln Asp Gln Ala Val	
50 55 60	
ctg cac cgg aac cgg gcc gcc tgc cac ctc aag ctg gaa gat tac gac	239
Leu His Arg Asn Arg Ala Ala Cys His Leu Lys Leu Glu Asp Tyr Asp	
65 70 75	
aaa gca gaa aca gag gca tcc aaa gcc att gaa aag gat ggt ggg gat	287
Lys Ala Glu Thr Glu Ala Ser Lys Ala Ile Glu Lys Asp Gly Gly Asp	
80 85 90 95	
gtc aaa gca ctc tac cgg cgg agc caa gcc cta gag aag ctg ggc cgc	335
Val Lys Ala Leu Tyr Arg Arg Ser Gln Ala Leu Glu Lys Leu Gly Arg	
100 105 110	
ctg gac cag gct gtc ctt gac ctg cag aga tgt gtg agc ttg gag ccc	383
Leu Asp Gln Ala Val Leu Asp Leu Gln Arg Cys Val Ser Leu Glu Pro	
115 120 125	
aag aac aaa gtt ttc cag gag gcc ttg cgg aac atc ggg ggc cag att	431
Lys Asn Lys Val Phe Gln Glu Ala Leu Arg Asn Ile Gly Gly Gln Ile	
130 135 140	
cag gag aag gtg cga tac atg tcc tcg acg gat gcc aaa gtg gaa cag	479
Gln Glu Lys Val Arg Tyr Met Ser Ser Thr Asp Ala Lys Val Glu Gln	
145 150 155	
atg ttt cag ata ctg ttg gac cca gaa gag aag ggc act gag aaa aag	527
Met Phe Gln Ile Leu Leu Asp Pro Glu Glu Lys Gly Thr Glu Lys Lys	
160 165 170 175	
caa aag gct tct cag aac ctg gtg gtg ctg gcc agg gag gat gct gga	575
Gln Lys Ala Ser Gln Asn Leu Val Val Leu Ala Arg Glu Asp Ala Gly	
180 185 190	
gcg gag aag atc ttc cgg agt aat ggg gtt cag ctc ttg caa cgt tta	623
Ala Glu Lys Ile Phe Arg Ser Asn Gly Val Gln Leu Leu Gln Arg Leu	
195 200 205	
ctg gac atg gga gag act gac ctc atg ctg gcg gct ctg cgt acg ctg	671
Leu Asp Met Gly Glu Thr Asp Leu Met Leu Ala Ala Leu Arg Thr Leu	
210 215 220	
gtt ggc att tgc tct gag cat cag tca cgg aca gtg gca acc ctg agc	719
Val Gly Ile Cys Ser Glu His Gln Ser Arg Thr Val Ala Thr Leu Ser	
225 230 235	
ata ctg gga act cgg cga gta gtc tcc atc ctg ggc gtg gaa agc cag	767
Ile Leu Gly Thr Arg Arg Val Val Ser Ile Leu Gly Val Glu Ser Gln	
240 245 250 255	
gct gtg tcc ctg gct gcc tgc cac ctg ctg cag gtt atg ttt gat gcc	815
Ala Val Ser Leu Ala Ala Cys His Leu Leu Gln Val Met Phe Asp Ala	
260 265 270	
ctc aag gaa ggt gtc aaa aaa ggc ttc cga ggc aaa gaa ggt gcc atc	863
Leu Lys Glu Gly Val Lys Lys Gly Phe Arg Gly Lys Glu Gly Ala Ile	
275 280 285	
att gtg gat cct gcc cgg gag ctg aag gtc ctc atc agt aac ctc tta	911
Ile Val Asp Pro Ala Arg Glu Leu Lys Val Leu Ile Ser Asn Leu Leu	
290 295 300	
gat ctg ctg aca gag gtg ggg gtc tct ggc caa ggc cga gac aat gcc	959
Asp Leu Leu Thr Glu Val Gly Val Ser Gly Gln Gly Arg Asp Asn Ala	
305 310 315	

ctg acc ctc ctg att aaa gcg gtg ccc cgg aag tct ctc aag gac ccc	1007
Leu Thr Leu Leu Ile Lys Ala Val Pro Arg Lys Ser Leu Lys Asp Pro	
320 325 330 335	
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Asn Asn Ser Leu Thr Leu Trp Val Ile Asp Gln Gly Leu Lys Lys Ile	
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ttg gaa gtg ggg ggc tct cta cag gac cct cct ggg gag ctc gca gtg	1103
Leu Glu Val Gly Gly Ser Leu Gln Asp Pro Pro Gly Glu Leu Ala Val	
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acc gca aac agc cgc atg agc gcc tct att ctc ctc agc aag ctc ttt	1151
Thr Ala Asn Ser Arg Met Ser Ala Ser Ile Leu Leu Ser Lys Leu Phe	
370 375 380	
gat gac ctc aag tgt gat gcg gag agg gag aat ttc cac aga ctt tgt	1199
Asp Asp Leu Lys Cys Asp Ala Glu Arg Glu Asn Phe His Arg Leu Cys	
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gaa aac tac atc aag agc tgg ttt gag ggc caa ggg ctg gcc ggg aag	1247
Glu Asn Tyr Ile Lys Ser Trp Phe Glu Gly Gln Gly Leu Ala Gly Lys	
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cta cgg gcc atc cag acg gtg tcc tgc ctc ctg cag ggc cca tgt gac	1295
Leu Arg Ala Ile Gln Thr Val Ser Cys Leu Leu Gln Gly Pro Cys Asp	
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gct ggc aac cgg gcc ttg gag ctg agc ggt gtc atg gag agt gtg att	1343
Ala Gly Asn Arg Ala Leu Glu Leu Ser Gly Val Met Glu Ser Val Ile	
435 440 445	
gct ctg tgt gcc tct gag cag gag gag gag cag ctg gtg gcc gtg gag	1391
Ala Leu Cys Ala Ser Glu Gln Glu Glu Glu Gln Leu Val Ala Val Glu	
450 455 460	
gct ctg atc cat gca gcc ggc aag gct aag cgg gcc tca ttc atc act	1439
Ala Leu Ile His Ala Ala Gly Lys Ala Lys Arg Ala Ser Phe Ile Thr	
465 470 475	
gcc aat ggt gtc tcg ctg ctg aag gac cta tat aag tgc agc gag aag	1487
Ala Asn Gly Val Ser Leu Leu Lys Asp Leu Tyr Lys Cys Ser Glu Lys	
480 485 490 495	
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Asp Ser Ile Arg Ile Arg Ala Leu Val Gly Leu Cys Lys Leu Gly Ser	
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gct gga ggg act gac ttc agc atg aag cag ttt gct gaa ggc tcc act	1583
Ala Gly Gly Thr Asp Phe Ser Met Lys Gln Phe Ala Glu Gly Ser Thr	
515 520 525	
ctc aaa ctg gct aag cag tgt cga aag tgg ctg tgc aat gac cag atc	1631
Leu Lys Leu Ala Lys Gln Cys Arg Lys Trp Leu Cys Asn Asp Gln Ile	
530 535 540	
gac gca ggc act cgg cgc tgg gca gtg gag ggc ctg gct tac ctg acc	1679
Asp Ala Gly Thr Arg Arg Trp Ala Val Glu Gly Leu Ala Tyr Leu Thr	
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ttt gat gcc gac gtg aag gaa gag ttt gtg gag gat gcg gct gct ctg	1727
Phe Asp Ala Asp Val Lys Glu Glu Phe Val Glu Asp Ala Ala Ala Leu	
560 565 570 575	
aaa gct ctg ttc cag ctc agc agg ttg gag gag agg tca gtg ctc ttt	1775
Lys Ala Leu Phe Gln Leu Ser Arg Leu Glu Glu Arg Ser Val Leu Phe	
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gcg gtg gcc tca gcg ctg gtg aac tgc acc aac agc tat gac tac gag	1823
Ala Val Ala Ser Ala Leu Val Asn Cys Thr Asn Ser Tyr Asp Tyr Glu	
595 600 605	
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Glu Pro Asp Pro Lys Met Val Glu Leu Ala Lys Tyr Ala Lys Gln His	
610 615 620	

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Val	Pro	Glu	Gln	His	Pro	Lys	Asp	Lys	Pro	Ser	Phe	Val	Arg	Ala	Arg	
	625						630				635					
gtg	aag	aag	ctg	ctg	gca	gcg	ggc	gtg	gtg	tcg	gcc	atg	gtg	tgc	atg	1967
Val	Lys	Lys	Leu	Leu	Ala	Ala	Gly	Val	Val	Ser	Ala	Met	Val	Cys	Met	
	640					645					650				655	
gtg	aag	acg	gag	agc	cct	gtg	ctg	acc	agt	tcc	tgc	aga	gag	ctg	ctc	2015
Val	Lys	Thr	Glu	Ser	Pro	Val	Leu	Thr	Ser	Ser	Cys	Arg	Glu	Leu	Leu	
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tcc	agg	gtc	ttc	ttg	gct	tta	gtg	gaa	gag	gta	gag	gac	cga	ggc	act	2063
Ser	Arg	Val	Phe	Leu	Ala	Leu	Val	Glu	Glu	Val	Glu	Asp	Arg	Gly	Thr	
			675						680				685			
gtg	gtt	gcc	cag	gga	ggc	ggc	agg	gcg	ctg	atc	ccg	ctg	gcc	ctg	gaa	2111
Val	Val	Ala	Gln	Gly	Gly	Gly	Arg	Ala	Leu	Ile	Pro	Leu	Ala	Leu	Glu	
		690						695					700			
ggc	acg	gac	gtg	ggg	cag	aca	aag	gca	gcc	cag	gcc	ctt	gcc	aag	ctc	2159
Gly	Thr	Asp	Val	Gly	Gln	Thr	Lys	Ala	Ala	Gln	Ala	Leu	Ala	Lys	Leu	
	705					710					715					
acc	atc	acc	tcc	aac	ccg	gag	atg	acc	ttc	cct	ggc	gag	cgg	atc	tat	2207
Thr	Ile	Thr	Ser	Asn	Pro	Glu	Met	Thr	Phe	Pro	Gly	Glu	Arg	Ile	Tyr	
	720				725					730					735	
gag	gtg	gtc	cgg	ccc	ctc	gtc	tcc	ctg	ttg	cac	ctc	aac	tgc	tca	ggc	2255
Glu	Val	Val	Arg	Pro	Leu	Val	Ser	Leu	Leu	His	Leu	Asn	Cys	Ser	Gly	
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ctg	cag	aac	ttc	gag	gcg	ctc	atg	gcc	cta	aca	aac	ctg	gct	ggg	atc	2303
Leu	Gln	Asn	Phe	Glu	Ala	Leu	Met	Ala	Leu	Thr	Asn	Leu	Ala	Gly	Ile	
			755						760					765		
agc	gag	agg	ctc	cgg	cag	aag	atc	ctg	aag	gag	aag	gct	gtg	ccc	atg	2351
Ser	Glu	Arg	Leu	Arg	Gln	Lys	Ile	Leu	Lys	Glu	Lys	Ala	Val	Pro	Met	
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Ile	Glu	Gly	Tyr	Met	Phe	Glu	Glu	His	Glu	Met	Ile	Arg	Arg	Ala	Ala	
	785						790					795				
acg	gag	tgc	atg	tgt	aac	ttg	gcc	atg	agc	aag	gag	gtg	cag	gac	ctc	2447
Thr	Glu	Cys	Met	Cys	Asn	Leu	Ala	Met	Ser	Lys	Glu	Val	Gln	Asp	Leu	
	800				805						810				815	
ttc	gaa	gcc	cag	ggc	aat	gac	cga	ctg	aag	ctg	ctg	gtg	ctg	tac	agt	2495
Phe	Glu	Ala	Gln	Gly	Asn	Asp	Arg	Leu	Lys	Leu	Leu	Val	Leu	Tyr	Ser	
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gga	gag	gat	gat	gag	ctg	cta	cag	cgg	gca	gct	gcc	ggg	ggc	ttg	gcc	2543
Gly	Glu	Asp	Asp	Glu	Leu	Leu	Gln	Arg	Ala	Ala	Ala	Gly	Gly	Leu	Ala	
				835					840					845		
atg	ctt	acc	tcc	atg	cgg	ccc	acg	ctc	tgc	agc	cgc	att	ccc	caa	gtg	2591
Met	Leu	Thr	Ser	Met	Arg	Pro	Thr	Leu	Cys	Ser	Arg	Ile	Pro	Gln	Val	
		850						855					860			
acc	aca	cac	tgg	ctg	gag	atc	ctg	cag	gcc	ctg	ctt	ctg	agc	tcc	aac	2639
Thr	Thr	His	Trp	Leu	Glu	Ile	Leu	Gln	Ala	Leu	Leu	Leu	Ser	Ser	Asn	
		865					870									
cag	gag	ctg	cag	cac	cgg	ggc	gct	gtg	gtg	gtg	ctg	aac	atg	gtg	gag	2687
Gln	Glu	Leu	Gln	His	Arg	Gly	Ala	Val	Val	Val	Leu	Asn	Met	Val	Glu	
	880					885					890				895	
gcc	tcg	agg	gag	att	gcc	agc	acc	ctg	atg	gag	agt	gag	atg	atg	gag	2735
Ala	Ser	Arg	Glu	Ile	Ala	Ser	Thr	Leu	Met	Glu	Ser	Glu	Met	Met	Glu	
				900						905					910	
atc	ttg	tca	gtg	cta	gct	aag	ggc	gac	cac	agc	cct	gtc	aca	agg	gct	2783
Ile	Leu	Ser	Val	Leu	Ala	Lys	Gly	Asp	His	Ser	Pro	Val	Thr	Arg	Ala	
			915					920							925	

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gct gca gcc tgc ctg gac aaa gca gtg gaa tat ggg ctt atc caa ccc 2831
Ala Ala Ala Cys Leu Asp Lys Ala Val Glu Tyr Gly Leu Ile Gln Pro
      930                      935                      940
aac caa gat gga gag tgagggggtt gtccctggggc ccaaggctca tgcacacgct 2886
Asn Gln Asp Gly Glu
      945
acctattgtg gcacggagag taaggacgga agcagctttg gctggtggtg gctggcatgc 2946
ccaatactct tgcccatcct cgcttgctgc cctaggatgt cctctgttct gagtcagcgg 3006
ccacgttcag tcacacagcc ctgcttggcc agcactgcct gcagcctcac tcagagggggc 3066
cctttttctg tactactgta gtcagctggg aatggggaag gtgcatccca acacagcctg 3126
tggatcctgg ggcatttgga agggcgacaca catcagcagc ctcaccagct gtgagcctgc 3186
tatcaggcct gccctccaa taaaagtgtg tagaactcc 3225

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<210> SEQ ID NO 14

<211> LENGTH: 948

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

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Leu Ser Ala Met Thr Ala Ser Ser Val Glu Gln Leu Arg Lys Glu Gly
      20          25          30
Asn Glu Leu Phe Lys Cys Gly Asp Tyr Gly Gly Ala Leu Ala Ala Tyr
      35          40          45
Thr Gln Ala Leu Gly Leu Asp Ala Thr Pro Gln Asp Gln Ala Val Leu
      50          55          60
His Arg Asn Arg Ala Ala Cys His Leu Lys Leu Glu Asp Tyr Asp Lys
      65          70          75          80
Ala Glu Thr Glu Ala Ser Lys Ala Ile Glu Lys Asp Gly Gly Asp Val
      85          90          95
Lys Ala Leu Tyr Arg Arg Ser Gln Ala Leu Glu Lys Leu Gly Arg Leu
      100          105          110
Asp Gln Ala Val Leu Asp Leu Gln Arg Cys Val Ser Leu Glu Pro Lys
      115          120          125
Asn Lys Val Phe Gln Glu Ala Leu Arg Asn Ile Gly Gly Gln Ile Gln
      130          135          140
Glu Lys Val Arg Tyr Met Ser Ser Thr Asp Ala Lys Val Glu Gln Met
      145          150          155          160
Phe Gln Ile Leu Leu Asp Pro Glu Glu Lys Gly Thr Glu Lys Lys Gln
      165          170          175
Lys Ala Ser Gln Asn Leu Val Val Leu Ala Arg Glu Asp Ala Gly Ala
      180          185          190
Glu Lys Ile Phe Arg Ser Asn Gly Val Gln Leu Leu Gln Arg Leu Leu
      195          200          205
Asp Met Gly Glu Thr Asp Leu Met Leu Ala Ala Leu Arg Thr Leu Val
      210          215          220
Gly Ile Cys Ser Glu His Gln Ser Arg Thr Val Ala Thr Leu Ser Ile
      225          230          235          240
Leu Gly Thr Arg Arg Val Val Ser Ile Leu Gly Val Glu Ser Gln Ala
      245          250          255
Val Ser Leu Ala Ala Cys His Leu Leu Gln Val Met Phe Asp Ala Leu
      260          265          270
Lys Glu Gly Val Lys Lys Gly Phe Arg Gly Lys Glu Gly Ala Ile Ile
      275          280          285
Val Asp Pro Ala Arg Glu Leu Lys Val Leu Ile Ser Asn Leu Leu Asp
      290          295          300
Leu Leu Thr Glu Val Gly Val Ser Gly Gln Gly Arg Asp Asn Ala Leu

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305					310					315				320
Thr	Leu	Leu	Ile	Lys	Ala	Val	Pro	Arg	Lys	Ser	Leu	Lys	Asp	Pro Asn
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Asn	Ser	Leu	Thr	Leu	Trp	Val	Ile	Asp	Gln	Gly	Leu	Lys	Lys	Ile Leu
			340					345					350	
Glu	Val	Gly	Gly	Ser	Leu	Gln	Asp	Pro	Pro	Gly	Glu	Leu	Ala	Val Thr
		355					360					365		
Ala	Asn	Ser	Arg	Met	Ser	Ala	Ser	Ile	Leu	Leu	Ser	Lys	Leu	Phe Asp
	370					375					380			
Asp	Leu	Lys	Cys	Asp	Ala	Glu	Arg	Glu	Asn	Phe	His	Arg	Leu	Cys Glu
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Asn	Tyr	Ile	Lys	Ser	Trp	Phe	Glu	Gly	Gln	Gly	Leu	Ala	Gly	Lys Leu
			405						410					415
Arg	Ala	Ile	Gln	Thr	Val	Ser	Cys	Leu	Leu	Gln	Gly	Pro	Cys	Asp Ala
			420					425					430	
Gly	Asn	Arg	Ala	Leu	Glu	Leu	Ser	Gly	Val	Met	Glu	Ser	Val	Ile Ala
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Leu	Cys	Ala	Ser	Glu	Gln	Glu	Glu	Glu	Gln	Leu	Val	Ala	Val	Glu Ala
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Leu	Ile	His	Ala	Ala	Gly	Lys	Ala	Lys	Arg	Ala	Ser	Phe	Ile	Thr Ala
465					470					475				480
Asn	Gly	Val	Ser	Leu	Leu	Lys	Asp	Leu	Tyr	Lys	Cys	Ser	Glu	Lys Asp
			485					490					495	
Ser	Ile	Arg	Ile	Arg	Ala	Leu	Val	Gly	Leu	Cys	Lys	Leu	Gly	Ser Ala
			500					505					510	
Gly	Gly	Thr	Asp	Phe	Ser	Met	Lys	Gln	Phe	Ala	Glu	Gly	Ser	Thr Leu
	515						520					525		
Lys	Leu	Ala	Lys	Gln	Cys	Arg	Lys	Trp	Leu	Cys	Asn	Asp	Gln	Ile Asp
	530					535					540			
Ala	Gly	Thr	Arg	Arg	Trp	Ala	Val	Glu	Gly	Leu	Ala	Tyr	Leu	Thr Phe
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Asp	Ala	Asp	Val	Lys	Glu	Glu	Phe	Val	Glu	Asp	Ala	Ala	Ala	Leu Lys
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Ala	Leu	Phe	Gln	Leu	Ser	Arg	Leu	Glu	Glu	Arg	Ser	Val	Leu	Phe Ala
			580					585					590	
Val	Ala	Ser	Ala	Leu	Val	Asn	Cys	Thr	Asn	Ser	Tyr	Asp	Tyr	Glu Glu
	595					600						605		
Pro	Asp	Pro	Lys	Met	Val	Glu	Leu	Ala	Lys	Tyr	Ala	Lys	Gln	His Val
	610					615					620			
Pro	Glu	Gln	His	Pro	Lys	Asp	Lys	Pro	Ser	Phe	Val	Arg	Ala	Arg Val
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Lys	Lys	Leu	Leu	Ala	Ala	Gly	Val	Val	Ser	Ala	Met	Val	Cys	Met Val
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Lys	Thr	Glu	Ser	Pro	Val	Leu	Thr	Ser	Ser	Cys	Arg	Glu	Leu	Leu Ser
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Arg	Val	Phe	Leu	Ala	Leu	Val	Glu	Glu	Val	Glu	Asp	Arg	Gly	Thr Val
		675					680					685		
Val	Ala	Gln	Gly	Gly	Gly	Arg	Ala	Leu	Ile	Pro	Leu	Ala	Leu	Glu Gly
	690					695					700			
Thr	Asp	Val	Gly	Gln	Thr	Lys	Ala	Ala	Gln	Ala	Leu	Ala	Lys	Leu Thr
705					710					715				720
Ile	Thr	Ser	Asn	Pro	Glu	Met	Thr	Phe	Pro	Gly	Glu	Arg	Ile	Tyr Glu
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Val	Val	Arg	Pro	Leu	Val	Ser	Leu	Leu	His	Leu	Asn	Cys	Ser	Gly Leu
			740					745					750	
Gln	Asn	Phe	Glu	Ala	Leu	Met	Ala	Leu	Thr	Asn	Leu	Ala	Gly	Ile Ser
	755						760						765	

Glu	Arg	Leu	Arg	Gln	Lys	Ile	Leu	Lys	Glu	Lys	Ala	Val	Pro	Met	Ile	
770						775					780					
Glu	Gly	Tyr	Met	Phe	Glu	Glu	His	Glu	Met	Ile	Arg	Arg	Ala	Ala	Thr	
785					790					795					800	
Glu	Cys	Met	Cys	Asn	Leu	Ala	Met	Ser	Lys	Glu	Val	Gln	Asp	Leu	Phe	
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Glu	Asp	Asp	Glu	Leu	Leu	Gln	Arg	Ala	Ala	Ala	Gly	Gly	Leu	Ala	Met	
		835					840					845				
Leu	Thr	Ser	Met	Arg	Pro	Thr	Leu	Cys	Ser	Arg	Ile	Pro	Gln	Val	Thr	
850						855					860					
Thr	His	Trp	Leu	Glu	Ile	Leu	Gln	Ala	Leu	Leu	Ser	Ser	Asn	Gln		
865					870					875				880		
Glu	Leu	Gln	His	Arg	Gly	Ala	Val	Val	Val	Leu	Asn	Met	Val	Glu	Ala	
				885					890					895		
Ser	Arg	Glu	Ile	Ala	Ser	Thr	Leu	Met	Glu	Ser	Glu	Met	Met	Glu	Ile	
			900					905					910			
Leu	Ser	Val	Leu	Ala	Lys	Gly	Asp	His	Ser	Pro	Val	Thr	Arg	Ala	Ala	
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Ala	Ala	Cys	Leu	Asp	Lys	Ala	Val	Glu	Tyr	Gly	Leu	Ile	Gln	Pro	Asn	
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Gln	Asp	Gly	Glu													
945																

<210> SEQ ID NO 15
 <211> LENGTH: 6002
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (326)..(5089)
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tgagataaac	tgatgaattg	gaacc atg	gtg caa	aag aag	ttc tgt	352
		Met Val	Gln Lys	Lys Lys	Phe Cys	Pro
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Arg Leu	Leu Asp	Tyr Leu	Val Ile	Val Gly	Ala Arg	400
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gat agc	gtg gcc	cag act	cct gaa	ttg cta	cgg cga	448
Asp Ser	Val Ala	Gln Thr	Pro Glu	Leu Leu	Arg Arg	448
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gat cac	act gag	ttt ccc	ctg ccc	cca gat	gta gtg	496
Asp His	Thr Glu	Phe Pro	Leu Pro	Pro Asp	Val Val	496
		45		50		55
ccc gag	ggc tgc	ctg agc	gtg cgg	cag cgg	cgc atg	544
Pro Glu	Gly Cys	Leu Ser	Val Arg	Gln Arg	Met Ser	544
		60		65		70
gat acc	tct ttt	gtc ttc	acc ctc	act gac	aag gac	592
Asp Thr	Ser Phe	Val Phe	Thr Leu	Thr Asp	Lys Asp	592
		75		80		85
cga tat	ggc atc	tgt gtt	aac ttc	tac cgc	tcc ttc	640

Arg 90	Tyr	Gly	Ile	Cys	Val	Asn	Phe	Tyr	Arg	Ser	Phe	Gln	Lys	Arg	Ile	
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Ser	Lys	Glu	Lys	Gly	Glu	Gly	Gly	Ala	Gly	Ser	Arg	Gly	Lys	Glu	Gly	
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acc	cat	gcc	acc	tgt	gcc	tca	gaa	gag	ggg	ggc	act	gag	agc	tca	gag	736
Thr	His	Ala	Thr	Cys	Ala	Ser	Glu	Glu	Gly	Gly	Thr	Glu	Ser	Ser	Glu	
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agt	ggc	tca	tcc	ctg	cag	cct	ctc	agt	gct	gac	tct	acc	cct	gat	gtg	784
Ser	Gly	Ser	Ser	Leu	Gln	Pro	Leu	Ser	Ala	Asp	Ser	Thr	Pro	Asp	Val	
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Asn	Gln	Ser	Pro	Arg	Gly	Lys	Arg	Arg	Ala	Lys	Ala	Gly	Ser	Arg	Ser	
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Arg	Asn	Ser	Thr	Leu	Thr	Ser	Leu	Cys	Val	Leu	Ser	His	Tyr	Pro	Phe	
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Phe	Ser	Thr	Phe	Arg	Glu	Cys	Leu	Tyr	Thr	Leu	Lys	Arg	Leu	Val	Asp	
				190					195					200		
tgc	tgt	agt	gag	cgc	ctt	ctg	ggc	aag	aaa	ctg	ggc	atc	cct	cga	ggc	976
Cys	Cys	Ser	Glu	Arg	Leu	Leu	Gly	Lys	Lys	Leu	Gly	Ile	Pro	Arg	Gly	
			205					210					215			
gta	caa	agg	gac	acc	atg	tgg	cgg	atc	ttt	act	gga	tcg	ctg	ctg	gta	1024
Val	Gln	Arg	Asp	Thr	Met	Trp	Arg	Ile	Phe	Thr	Gly	Ser	Leu	Leu	Val	
			220				225					230				
gag	gag	aag	tca	agt	gcc	ctt	ctg	cat	gac	ctt	cga	gag	att	gag	gcc	1072
Glu	Glu	Lys	Ser	Ser	Ala	Leu	Leu	His	Asp	Leu	Arg	Glu	Ile	Glu	Ala	
			235			240					245					
tgg	atc	tat	cga	ttg	ctg	cgc	tcc	cca	gta	ccc	gtc	tct	ggg	cag	aag	1120
Trp	Ile	Tyr	Arg	Leu	Leu	Arg	Ser	Pro	Val	Pro	Val	Ser	Gly	Gln	Lys	
				255						260				265		
cga	gta	gac	atc	gag	gtc	cta	ccc	caa	gag	ctc	cag	cca	gct	ctg	acc	1168
Arg	Val	Asp	Ile	Glu	Val	Leu	Pro	Gln	Glu	Leu	Gln	Pro	Ala	Leu	Thr	
				270					275					280		
ttt	gct	ctt	cca	gac	cca	tct	cga	ttc	acc	cta	gtg	gat	ttc	cca	ctg	1216
Phe	Ala	Leu	Pro	Asp	Pro	Ser	Arg	Phe	Thr	Leu	Val	Asp	Phe	Pro	Leu	
			285					290					295			
cac	ctt	ccc	ttg	gaa	ctt	cta	ggg	gtg	gac	gcc	tgt	ctc	cag	gtg	cta	1264
His	Leu	Pro	Leu	Glu	Leu	Leu	Gly	Val	Asp	Ala	Cys	Leu	Gln	Val	Leu	
			300				305					310				
acc	tgc	att	ctg	tta	gag	cac	aag	gtg	gtg	cta	cag	tcc	cga	gac	tac	1312
Thr	Cys	Ile	Leu	Leu	Glu	His	Lys	Val	Val	Leu	Gln	Ser	Arg	Asp	Tyr	
			315				320					325				
aat	gca	ctc	tcc	atg	tct	gtg	atg	gca	ttc	gtg	gca	atg	atc	tac	cca	1360
Asn	Ala	Leu	Ser	Met	Ser	Val	Met	Ala	Phe	Val	Ala	Met	Ile	Tyr	Pro	
330					335					340					345	
ctg	gaa	tat	atg	ttt	cct	gtc	atc	ccg	ctg	cta	ccc	acc	tgc	atg	gca	1408
Leu	Glu	Tyr	Met	Phe	Pro	Val	Ile	Pro	Leu	Leu	Pro	Thr	Cys	Met	Ala	
				350					355					360		
tca	gca	gag	cag	ctg	ctg	ttg	gct	cca	acc	ccg	tac	atc	att	ggg	gtt	1456
Ser	Ala	Glu	Gln	Leu	Leu	Leu	Ala	Pro	Thr	Pro	Tyr	Ile	Ile	Gly	Val	
				365				370						375		
cct	gcc	agc	ttc	ttc	ctc	tac	aaa	ctg	gac	ttc	aaa	atg	cct	gat	gat	1504
Pro	Ala	Ser	Phe	Phe	Leu	Tyr	Lys	Leu	Asp	Phe	Lys	Met	Pro	Asp	Asp	
			380				385						390			
gta	tgg	cta	gtg	gat	ctg	gac	agc	aat	agg	gtg	att	gcc	ccc	acc	aat	1552

Val	Trp	Leu	Val	Asp	Leu	Asp	Ser	Asn	Arg	Val	Ile	Ala	Pro	Thr	Asn	
395						400					405					
gca	gaa	gtg	ctg	cct	atc	ctg	cca	gaa	cca	gaa	tca	cta	gag	ctg	aaa	1600
Ala	Glu	Val	Leu	Pro	Ile	Leu	Pro	Glu	Pro	Glu	Ser	Leu	Glu	Leu	Lys	
410					415					420					425	
aag	cat	tta	aag	cag	gcc	ttg	gcc	agc	atg	agt	ctc	aac	acc	cag	ccc	1648
Lys	His	Leu	Lys	Gln	Ala	Leu	Ala	Ser	Met	Ser	Leu	Asn	Thr	Gln	Pro	
				430					435					440		
atc	ctc	aat	ctg	gag	aaa	ttt	cat	gag	ggc	cag	gag	atc	ccc	ctt	ctc	1696
Ile	Leu	Asn	Leu	Glu	Lys	Phe	His	Glu	Gly	Gln	Glu	Ile	Pro	Leu	Leu	
				445				450					455			
ttg	gga	agg	cct	tct	aat	gac	ctg	cag	tcc	aca	ccg	tcc	act	gaa	ttc	1744
Leu	Gly	Arg	Pro	Ser	Asn	Asp	Leu	Gln	Ser	Thr	Pro	Ser	Thr	Glu	Phe	
			460				465					470				
aac	cca	ctc	atc	tat	ggc	aat	gat	gtg	gat	tct	gtg	gat	gtt	gca	acc	1792
Asn	Pro	Leu	Ile	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Val	Asp	Val	Ala	Thr	
	475					480					485					
agg	gtt	gcc	atg	gta	cgg	ttc	ttc	aat	tcc	gcc	aac	gtg	ctg	cag	gga	1840
Arg	Val	Ala	Met	Val	Arg	Phe	Phe	Asn	Ser	Ala	Asn	Val	Leu	Gln	Gly	
490					495					500					505	
ttt	cag	atg	cac	acg	cgt	acc	ctg	cgc	ctc	ttt	cct	cgg	cct	gtg	gta	1888
Phe	Gln	Met	His	Thr	Arg	Thr	Leu	Arg	Leu	Phe	Pro	Arg	Pro	Val	Val	
				510					515					520		
gct	ttt	caa	gct	ggc	tcc	ttt	cta	gcc	tca	cgt	ccc	cgg	cag	act	cct	1936
Ala	Phe	Gln	Ala	Gly	Ser	Phe	Leu	Ala	Ser	Arg	Pro	Arg	Gln	Thr	Pro	
				525				530					535			
ttt	gcc	gag	aaa	ttg	gcc	agg	act	cag	gct	gtg	gag	tac	ttt	ggg	gaa	1984
Phe	Ala	Glu	Lys	Leu	Ala	Arg	Thr	Gln	Ala	Val	Glu	Tyr	Phe	Gly	Glu	
	540					545					550					
tgg	atc	ctt	aac	ccc	acc	aac	tat	gcc	ttt	cag	cga	att	cac	aac	aat	2032
Trp	Ile	Leu	Asn	Pro	Thr	Asn	Tyr	Ala	Phe	Gln	Arg	Ile	His	Asn	Asn	
	555					560					565					
atg	ttt	gat	cca	gcc	ctg	att	ggg	gac	aag	cca	aag	tgg	tat	gct	cat	2080
Met	Phe	Asp	Pro	Ala	Leu	Ile	Gly	Asp	Lys	Pro	Lys	Trp	Tyr	Ala	His	
570					575					580					585	
cag	ctg	cag	cct	atc	cac	tat	cgc	gtc	tat	gac	agc	aat	tcc	cag	ctg	2128
Gln	Leu	Gln	Pro	Ile	His	Tyr	Arg	Val	Tyr	Asp	Ser	Asn	Ser	Gln	Leu	
				590					595					600		
gct	gag	gcc	ctg	agt	gta	cca	cca	gag	cgg	gac	tct	gac	tcc	gaa	cct	2176
Ala	Glu	Ala	Leu	Ser	Val	Pro	Pro	Glu	Arg	Asp	Ser	Asp	Ser	Glu	Pro	
			605					610					615			
act	gat	gat	agt	ggc	agt	gat	agt	atg	gat	tat	gac	gat	tca	agc	tct	2224
Thr	Asp	Asp	Ser	Gly	Ser	Asp	Ser	Met	Asp	Tyr	Asp	Asp	Ser	Ser	Ser	
			620				625					630				
tct	tac	tcc	tcc	ctt	ggg	gac	ttt	gtc	agt	gaa	atg	atg	aaa	tgt	gac	2272
Ser	Tyr	Ser	Ser	Leu	Gly	Asp	Phe	Val	Ser	Glu	Met	Met	Lys	Cys	Asp	
	635					640					645					
att	aat	ggg	gat	act	ccc	aat	gtg	gac	cct	ctg	aca	cat	gca	gca	ctg	2320
Ile	Asn	Gly	Asp	Thr	Pro	Asn	Val	Asp	Pro	Leu	Thr	His	Ala	Ala	Leu	
650					655					660					665	
ggg	gat	gcc	agc	gag	gtg	gag	att	gac	gag	ctg	cag	aat	cag	aag	gaa	2368
Gly	Asp	Ala	Ser	Glu	Val	Glu	Ile	Asp	Glu	Leu	Gln	Asn	Gln	Lys	Glu	
				670					675					680		
gca	gaa	gag	cct	ggc	cca	gac	agt	gag	aac	tct	cag	gaa	aac	ccc	cca	2416
Ala	Glu	Glu	Pro	Gly	Pro	Asp	Ser	Glu	Asn	Ser	Gln	Glu	Asn	Pro	Pro	
			685					690					695			
ctg	cgc	tcc	agc	tct	agc	acc	aca	gcc	agc	agc	agc	ccc	agc	act	gtc	2464

Leu	Arg	Ser	Ser	Ser	Ser	Thr	Thr	Ala	Ser	Ser	Ser	Pro	Ser	Thr	Val	
		700						705				710				
atc	cac	gga	gcc	aac	tct	gaa	cct	gct	gac	tct	acg	gag	atg	gat	gat	2512
Ile	His	Gly	Ala	Asn	Ser	Glu	Pro	Ala	Asp	Ser	Thr	Glu	Met	Asp	Asp	
		715						720				725				
aag	gca	gca	gta	ggc	gtc	tcc	aag	ccc	ctc	cct	tcc	gtg	cct	ccc	agc	2560
Lys	Ala	Ala	Val	Gly	Val	Ser	Lys	Pro	Leu	Pro	Ser	Val	Pro	Pro	Ser	
		730						735				740			745	
att	ggc	aaa	tcg	aac	atg	gac	aga	cgt	cag	gca	gaa	att	gga	gag	ggg	2608
Ile	Gly	Lys	Ser	Asn	Met	Asp	Arg	Arg	Gln	Ala	Glu	Ile	Gly	Glu	Gly	
				750					755						760	
tca	gtg	cgc	cgg	cga	atc	tat	gac	aat	cca	tac	ttc	gag	ccc	caa	tat	2656
Ser	Val	Arg	Arg	Arg	Ile	Tyr	Asp	Asn	Pro	Tyr	Phe	Glu	Pro	Gln	Tyr	
				765					770						775	
ggc	ttt	ccc	cct	gag	gaa	gat	gag	gat	gag	cag	ggg	gaa	agt	tac	act	2704
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		780							785						790	
ccc	cga	ttc	agc	caa	cat	gtc	agt	ggc	aat	cgg	gct	caa	aag	ctg	ctg	2752
Pro	Arg	Phe	Ser	Gln	His	Val	Ser	Gly	Asn	Arg	Ala	Gln	Lys	Leu	Leu	
		795						800							805	
cgg	ccc	aac	agc	ttg	aga	ctg	gca	agt	gac	tca	gat	gca	gag	tca	gac	2800
Arg	Pro	Asn	Ser	Leu	Arg	Leu	Ala	Ser	Asp	Ser	Asp	Ala	Glu	Ser	Asp	
				810											825	
tct	cgg	gca	agc	tct	ccc	aac	tcc	acc	gtc	tcc	aac	acc	agc	acc	gag	2848
Ser	Arg	Ala	Ser	Ser	Pro	Asn	Ser	Thr	Val	Ser	Asn	Thr	Ser	Thr	Glu	
				830											840	
ggc	ttc	ggg	ggc	atc	atg	tct	ttt	gcc	agc	agc	ctc	tat	cgg	aac	cac	2896
Gly	Phe	Gly	Gly	Ile	Met	Ser	Phe	Ala	Ser	Ser	Leu	Tyr	Arg	Asn	His	
				845											855	
agt	acc	agc	ttc	agt	ctt	tca	aac	ctc	aca	ctg	ccc	acc	aaa	ggg	gcc	2944
Ser	Thr	Ser	Phe	Ser	Leu	Ser	Asn	Leu	Thr	Leu	Pro	Thr	Lys	Gly	Ala	
				860											870	
cga	gag	aag	gcc	acg	ccc	ttc	ccc	agt	ctg	aaa	gga	aac	agg	agg	gcg	2992
Arg	Glu	Lys	Ala	Thr	Pro	Phe	Pro	Ser	Leu	Lys	Gly	Asn	Arg	Arg	Ala	
				875											885	
tta	gtg	gat	cag	aag	tca	tct	gtc	att	aaa	cac	agc	cca	aca	gtg	aaa	3040
Leu	Val	Asp	Gln	Lys	Ser	Ser	Val	Ile	Lys	His	Ser	Pro	Thr	Val	Lys	
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aga	gaa	cct	cca	tca	ccc	cag	ggg	cga	tcc	agc	aac	tct	agt	gag	aac	3088
Arg	Glu	Pro	Pro	Ser	Pro	Gln	Gly	Arg	Ser	Ser	Asn	Ser	Ser	Glu	Asn	
				910											920	
cag	cag	ttc	ctg	aag	gag	gtg	gtg	cac	agc	gtg	ctg	gac	ggc	cag	gga	3136
Gln	Gln	Phe	Leu	Lys	Glu	Val	Val	His	Ser	Val	Leu	Asp	Gly	Gln	Gly	
				925											935	
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Val	Gly	Trp	Leu	Asn	Met	Lys	Lys	Val	Arg	Arg	Leu	Leu	Glu	Ser	Glu	
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cag	ctg	cga	gtc	ttt	gtc	ctg	agc	aag	ctg	aac	cgc	atg	gtg	cag	tca	3232
Gln	Leu	Arg	Val	Phe	Val	Leu	Ser	Lys	Leu	Asn	Arg	Met	Val	Gln	Ser	
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gag	gac	gat	gcc	cgg	cag	gac	atc	atc	ccg	gat	gtg	gag	atc	agt	cgg	3280
Glu	Asp	Asp	Ala	Arg	Gln	Asp	Ile	Ile	Pro	Asp	Val	Glu	Ile	Ser	Arg	
				970											985	
aag	gtg	tac	aag	gga	atg	tta	gac	ctc	ctc	aag	tgt	aca	gtc	ctc	agc	3328
Lys	Val	Tyr	Lys	Gly	Met	Leu	Asp	Leu	Leu	Lys	Cys	Thr	Val	Leu	Ser	
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Leu	Glu	Gln	Ser	Tyr	Ala	His	Ala	Gly	Leu	Gly	Gly	Met	Ala	Ser	Ile		
			1005					1010					1015				
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Phe	Gly	Leu	Leu	Glu	Ile	Ala	Gln	Thr	His	Tyr	Tyr	Ser	Lys	Glu	Pro		
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Asp	Lys	Arg	Lys	Arg	Ser	Pro	Thr	Glu	Ser	Val	Asn	Thr	Pro	Val	Gly		
			1035					1040					1045				
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Lys	Asp	Pro	Gly	Leu	Ala	Gly	Arg	Gly	Asp	Pro	Lys	Ala	Met	Ala	Gln		
			1050					1055					1060			1065	
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Leu	Arg	Val	Pro	Gln	Leu	Gly	Pro	Arg	Ala	Pro	Ser	Ala	Thr	Gly	Lys		
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ggt	cct	aag	gaa	ctg	gac	acc	aga	agt	tta	aag	gaa	gaa	aat	ttt	ata	3616	
Gly	Pro	Lys	Glu	Leu	Asp	Thr	Arg	Ser	Leu	Lys	Glu	Glu	Asn	Phe	Ile		
			1085							1090					1095		
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Ala	Ser	Ile	Gly	Pro	Glu	Val	Ile	Lys	Pro	Val	Phe	Asp	Leu	Gly	Glu		
			1100					1105					1110				
aca	gag	gag	aaa	aag	tcc	cag	atc	agc	gca	gac	agt	ggt	gtg	agc	ctg	3712	
Thr	Glu	Glu	Lys	Lys	Ser	Gln	Ile	Ser	Ala	Asp	Ser	Gly	Val	Ser	Leu		
			1115					1120					1125				
acg	tct	agt	tcc	cag	agg	act	gat	caa	gac	tct	gtc	atc	ggc	gtg	agt	3760	
Thr	Ser	Ser	Ser	Gln	Arg	Thr	Asp	Gln	Asp	Ser	Val	Ile	Gly	Val	Ser		
				1130				1135					1140			1145	
cca	gct	gtt	atg	atc	cgc	agc	tca	agt	cag	gat	tct	gaa	gtt	agc	acc	3808	
Pro	Ala	Val	Met	Ile	Arg	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Val	Ser	Thr		
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Val	Val	Ser	Asn	Ser	Ser	Gly	Glu	Thr	Leu	Gly	Ala	Asp	Ser	Asp	Leu		
			1165					1170					1175				
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Ser	Ser	Asn	Ala	Gly	Asp	Gly	Pro	Gly	Gly	Glu	Gly	Ser	Val	His	Leu		
			1180					1185					1190				
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Ala	Ser	Ser	Arg	Gly	Thr	Leu	Ser	Asp	Ser	Glu	Ile	Glu	Thr	Asn	Ser		
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gcc	aca	agc	acc	atc	ttt	ggt	aaa	gcc	cac	agc	ttg	aag	cca	agc	ata	4000	
Ala	Thr	Ser	Thr	Ile	Phe	Gly	Lys	Ala	His	Ser	Leu	Lys	Pro	Ser	Ile		
			1210					1215					1220			1225	
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Lys	Glu	Lys	Leu	Ala	Gly	Ser	Pro	Ile	Arg	Thr	Ser	Glu	Asp	Val	Ser		
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Gln	Arg	Val	Tyr	Leu	Tyr	Glu	Gly	Leu	Leu	Gly	Lys	Glu	Arg	Ser	Thr		
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Leu	Trp	Asp	Gln	Met	Gln	Phe	Trp	Glu	Asp	Ala	Phe	Leu	Asp	Ala	Val		
			1260					1265					1270				
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Met	Leu	Glu	Arg	Glu	Gly	Met	Gly	Met	Asp	Gln	Gly	Pro	Gln	Glu	Met		
			1275					1280					1285				
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Ile	Asp	Arg	Tyr	Leu	Ser	Leu	Gly	Glu	His	Asp	Arg	Lys	Arg	Leu	Glu		
			1290					1295					1300			1305	
gat	gat	gaa	gat	cgc	ttg	ctg	gcc	aca	ctt	ctg	cac	aac	ctc	atc	tcc	4288	

Asp Asp Glu Asp Arg Leu Leu Ala Thr Leu Leu His Asn Leu Ile Ser	
1310 1315 1320	
tac atg ctg ctg atg aag gta aat aag aat gac atc cgc aag aag gtg	4336
Tyr Met Leu Leu Met Lys Val Asn Lys Asn Asp Ile Arg Lys Lys Val	
1325 1330 1335	
agg cgc cta atg gga aag tcg cac att ggg ctt gtg tac agc cag caa	4384
Arg Arg Leu Met Gly Lys Ser His Ile Gly Leu Val Tyr Ser Gln Gln	
1340 1345 1350	
atc aat gag gtg ctt gat cag ctg gcg aac ctg aat gga cgc gat ctc	4432
Ile Asn Glu Val Leu Asp Gln Leu Ala Asn Leu Asn Gly Arg Asp Leu	
1355 1360 1365	
tct atc tgg tcc agt ggc agc cgg cac atg aag aag cag aca ttt gtg	4480
Ser Ile Trp Ser Ser Arg His Met Lys Lys Gln Thr Phe Val	
1370 1375 1380 1385	
gta cat gca ggg aca gat aca aac gga gat atc ttt ttc atg gag gtg	4528
Val His Ala Gly Thr Asp Thr Asn Gly Asp Ile Phe Phe Met Glu Val	
1390 1395 1400	
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Cys Asp Asp Cys Val Val Leu Arg Ser Asn Ile Gly Thr Val Tyr Glu	
1405 1410 1415	
cgc tgg tgg tac gag aag ctc atc aac atg acc tac tgt ccc aag acg	4624
Arg Trp Trp Tyr Glu Lys Leu Ile Asn Met Thr Tyr Cys Pro Lys Thr	
1420 1425 1430	
aag gtg ttg tgc ttg tgg cgt aga aat ggc tct gag acc cag ctc aac	4672
Lys Val Leu Cys Leu Trp Arg Arg Asn Gly Ser Glu Thr Gln Leu Asn	
1435 1440 1445	
aag ttc tat act aaa aag tgt cgg gag ctg tac tac tgt gtg aag gac	4720
Lys Phe Tyr Thr Lys Lys Cys Arg Glu Leu Tyr Tyr Cys Val Lys Asp	
1450 1455 1460 1465	
agc atg gag cgc gct gcc gcc cga cag caa agc atc aaa ccc gga cct	4768
Ser Met Glu Arg Ala Ala Ala Arg Gln Gln Ser Ile Lys Pro Gly Pro	
1470 1475 1480	
gaa ttg ggt ggc gag ttc cct gtg cag gac ctg aag act ggt gag ggt	4816
Glu Leu Gly Gly Glu Phe Pro Val Gln Asp Leu Lys Thr Gly Glu Gly	
1485 1490 1495	
ggc ctg ctg cag gtg acc ctg gaa ggg atc aac ctc aaa ttc atg cac	4864
Gly Leu Leu Gln Val Thr Leu Glu Gly Ile Asn Leu Lys Phe Met His	
1500 1505 1510	
aat cag gtt ttc ata gag ctg aat cac att aaa aag tgc aat aca gtt	4912
Asn Gln Val Phe Ile Glu Leu Asn His Ile Lys Lys Cys Asn Thr Val	
1515 1520 1525	
cga ggc gtc ttt gtc ctg gag gaa ttt gtt cct gaa att aaa gaa gtg	4960
Arg Gly Val Phe Val Leu Glu Glu Phe Val Pro Glu Ile Lys Glu Val	
1530 1535 1540 1545	
gtg agc cac aag tac aag aca cca atg gcc cac gaa atc tgc tac tcc	5008
Val Ser His Lys Tyr Lys Thr Pro Met Ala His Glu Ile Cys Tyr Ser	
1550 1555 1560	
gta tta tgt ctc ttc tcg tac gtg gct gca gtt cat agc agt gag gaa	5056
Val Leu Cys Leu Phe Ser Tyr Val Ala Ala Val His Ser Ser Glu Glu	
1565 1570 1575	
gat ctc aga acc ccg ccc cgg cct gtc tct agc tgatggagag gggctacgca	5109
Asp Leu Arg Thr Pro Pro Arg Pro Val Ser Ser	
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ggttaccggg tatgtgtccc tctgagtgtg tcttgagcgt gtccaccttc tccctctcca	5289
ctcccagaag accaaaactgc cttccccctca gggctcaaga atgtgtacag tctgtggggc	5349

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cggtgtgaac ccactatttt gtgtccttga gacatttgtg ttgtgggttcc ttgtccttgt 5409
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gactggggcgc ctggagcagt ttcactctgt gaggagttag ggaaccctgg ggctcaccct 5529
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gctgctgcct gccacagcct ctgtgactgc agtggagcgg cgaattccct gtggcctgcc 5709
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gaaatgactg taaatatttc agccccacat tatttataga aaatgtacag ttgtgtgaat 5949
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<210> SEQ ID NO 16

<211> LENGTH: 1588

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

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Met Val Gln Lys Lys Lys Phe Cys Pro Arg Leu Leu Asp Tyr Leu Val
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Ile Val Gly Ala Arg His Pro Ser Ser Asp Ser Val Ala Gln Thr Pro
          20             25             30
Glu Leu Leu Arg Arg Tyr Pro Leu Glu Asp His Thr Glu Phe Pro Leu
          35             40             45
Pro Pro Asp Val Val Phe Phe Cys Gln Pro Glu Gly Cys Leu Ser Val
          50             55             60
Arg Gln Arg Arg Met Ser Leu Arg Asp Asp Thr Ser Phe Val Phe Thr
          65             70             75             80
Leu Thr Asp Lys Asp Thr Gly Val Thr Arg Tyr Gly Ile Cys Val Asn
          85             90             95
Phe Tyr Arg Ser Phe Gln Lys Arg Ile Ser Lys Glu Lys Gly Glu Gly
          100            105            110
Gly Ala Gly Ser Arg Gly Lys Glu Gly Thr His Ala Thr Cys Ala Ser
          115            120            125
Glu Glu Gly Gly Thr Glu Ser Ser Glu Ser Gly Ser Ser Leu Gln Pro
          130            135            140
Leu Ser Ala Asp Ser Thr Pro Asp Val Asn Gln Ser Pro Arg Gly Lys
          145            150            155            160
Arg Arg Ala Lys Ala Gly Ser Arg Ser Arg Asn Ser Thr Leu Thr Ser
          165            170            175
Leu Cys Val Leu Ser His Tyr Pro Phe Phe Ser Thr Phe Arg Glu Cys
          180            185            190
Leu Tyr Thr Leu Lys Arg Leu Val Asp Cys Cys Ser Glu Arg Leu Leu
          195            200            205
Gly Lys Lys Leu Gly Ile Pro Arg Gly Val Gln Arg Asp Thr Met Trp
          210            215            220
Arg Ile Phe Thr Gly Ser Leu Leu Val Glu Glu Lys Ser Ser Ala Leu
          225            230            235            240
Leu His Asp Leu Arg Glu Ile Glu Ala Trp Ile Tyr Arg Leu Leu Arg
          245            250            255
Ser Pro Val Pro Val Ser Gly Gln Lys Arg Val Asp Ile Glu Val Leu
          260            265            270
Pro Gln Glu Leu Gln Pro Ala Leu Thr Phe Ala Leu Pro Asp Pro Ser
          275            280            285
Arg Phe Thr Leu Val Asp Phe Pro Leu His Leu Pro Leu Glu Leu Leu
          290            295            300
Gly Val Asp Ala Cys Leu Gln Val Leu Thr Cys Ile Leu Leu Glu His
          305            310            315            320

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Lys	Val	Val	Leu	Gln	Ser	Arg	Asp	Tyr	Asn	Ala	Leu	Ser	Met	Ser	Val	
				325					330					335		
Met	Ala	Phe	Val	Ala	Met	Ile	Tyr	Pro	Leu	Glu	Tyr	Met	Phe	Pro	Val	
			340					345					350			
Ile	Pro	Leu	Leu	Pro	Thr	Cys	Met	Ala	Ser	Ala	Glu	Gln	Leu	Leu	Leu	
		355					360					365				
Ala	Pro	Thr	Pro	Tyr	Ile	Ile	Gly	Val	Pro	Ala	Ser	Phe	Phe	Leu	Tyr	
	370					375				380						
Lys	Leu	Asp	Phe	Lys	Met	Pro	Asp	Asp	Val	Trp	Leu	Val	Asp	Leu	Asp	
385					390					395				400		
Ser	Asn	Arg	Val	Ile	Ala	Pro	Thr	Asn	Ala	Glu	Val	Leu	Pro	Ile	Leu	
			405						410					415		
Pro	Glu	Pro	Glu	Ser	Leu	Glu	Leu	Lys	Lys	His	Leu	Lys	Gln	Ala	Leu	
			420				425						430			
Ala	Ser	Met	Ser	Leu	Asn	Thr	Gln	Pro	Ile	Leu	Asn	Leu	Glu	Lys	Phe	
		435					440					445				
His	Glu	Gly	Gln	Glu	Ile	Pro	Leu	Leu	Leu	Gly	Arg	Pro	Ser	Asn	Asp	
	450					455					460					
Leu	Gln	Ser	Thr	Pro	Ser	Thr	Glu	Phe	Asn	Pro	Leu	Ile	Tyr	Gly	Asn	
465					470					475					480	
Asp	Val	Asp	Ser	Val	Asp	Val	Ala	Thr	Arg	Val	Ala	Met	Val	Arg	Phe	
			485						490					495		
Phe	Asn	Ser	Ala	Asn	Val	Leu	Gln	Gly	Phe	Gln	Met	His	Thr	Arg	Thr	
			500					505					510			
Leu	Arg	Leu	Phe	Pro	Arg	Pro	Val	Val	Ala	Phe	Gln	Ala	Gly	Ser	Phe	
		515					520					525				
Leu	Ala	Ser	Arg	Pro	Arg	Gln	Thr	Pro	Phe	Ala	Glu	Lys	Leu	Ala	Arg	
	530					535					540					
Thr	Gln	Ala	Val	Glu	Tyr	Phe	Gly	Glu	Trp	Ile	Leu	Asn	Pro	Thr	Asn	
545					550					555					560	
Tyr	Ala	Phe	Gln	Arg	Ile	His	Asn	Asn	Met	Phe	Asp	Pro	Ala	Leu	Ile	
			565						570					575		
Gly	Asp	Lys	Pro	Lys	Trp	Tyr	Ala	His	Gln	Leu	Gln	Pro	Ile	His	Tyr	
			580					585					590			
Arg	Val	Tyr	Asp	Ser	Asn	Ser	Gln	Leu	Ala	Glu	Ala	Leu	Ser	Val	Pro	
		595					600					605				
Pro	Glu	Arg	Asp	Ser	Asp	Ser	Glu	Pro	Thr	Asp	Asp	Ser	Gly	Ser	Asp	
	610					615						620				
Ser	Met	Asp	Tyr	Asp	Asp	Ser	Ser	Ser	Ser	Tyr	Ser	Ser	Leu	Gly	Asp	
625					630					635				640		
Phe	Val	Ser	Glu	Met	Met	Lys	Cys	Asp	Ile	Asn	Gly	Asp	Thr	Pro	Asn	
			645						650					655		
Val	Asp	Pro	Leu	Thr	His	Ala	Ala	Leu	Gly	Asp	Ala	Ser	Glu	Val	Glu	
			660					665					670			
Ile	Asp	Glu	Leu	Gln	Asn	Gln	Lys	Glu	Ala	Glu	Glu	Pro	Gly	Pro	Asp	
	675						680					685				
Ser	Glu	Asn	Ser	Gln	Glu	Asn	Pro	Pro	Leu	Arg	Ser	Ser	Ser	Ser	Thr	
	690					695					700					
Thr	Ala	Ser	Ser	Ser	Pro	Ser	Thr	Val	Ile	His	Gly	Ala	Asn	Ser	Glu	
705					710					715					720	
Pro	Ala	Asp	Ser	Thr	Glu	Met	Asp	Asp	Lys	Ala	Ala	Val	Gly	Val	Ser	
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Lys	Pro	Leu	Pro	Ser	Val	Pro	Pro	Ser	Ile	Gly	Lys	Ser	Asn	Met	Asp	
			740					745					750			
Arg	Arg	Gln	Ala	Glu	Ile	Gly	Glu	Gly	Ser	Val	Arg	Arg	Arg	Ile	Tyr	
		755					760					765				
Asp	Asn	Pro	Tyr	Phe	Glu	Pro	Gln	Tyr	Gly	Phe	Pro	Pro	Glu	Glu	Asp	

770					775					780					
Glu Asp	Glu Gln	Gly	Glu Ser	Tyr Thr	Pro Arg	Phe Ser	Gln His	Val							
785			790		795			800							
Ser Gly	Asn Arg	Ala Gln	Lys Leu	Leu Arg	Pro Asn	Ser Leu	Arg Leu								
		805			810			815							
Ala Ser	Asp Ser	Asp Ala	Glu Ser	Asp Ser	Arg Ala	Ser Ser	Pro Asn								
		820			825			830							
Ser Thr	Val Ser	Asn Thr	Ser Thr	Glu Gly	Phe Gly	Gly Ile	Met Ser								
		835			840			845							
Phe Ala	Ser Ser	Leu Tyr	Arg Asn	His Ser	Thr Ser	Phe Ser	Leu Ser								
		850			855			860							
Asn Leu	Thr Leu	Pro Thr	Lys Gly	Ala Arg	Glu Lys	Ala Thr	Pro Phe								
865			870		875			880							
Pro Ser	Leu Lys	Gly Asn	Arg Arg	Ala Leu	Val Asp	Gln Lys	Ser Ser								
		885			890			895							
Val Ile	Lys His	Ser Pro	Thr Val	Lys Arg	Glu Pro	Pro Ser	Gln								
		900			905			910							
Gly Arg	Ser Ser	Asn Ser	Ser Ser	Glu Asn	Gln Gln	Phe Leu	Lys Glu	Val							
		915			920			925							
Val His	Ser Val	Leu Asp	Gly Gln	Gly Val	Gly Trp	Leu Asn	Met Lys								
		930			935			940							
Lys Val	Arg Arg	Leu Leu	Glu Ser	Glu Gln	Leu Arg	Val Phe	Val Leu								
945			950		955			960							
Ser Lys	Leu Asn	Arg Met	Val Gln	Ser Glu	Asp Asp	Ala Arg	Gln Asp								
		965			970			975							
Ile Ile	Pro Asp	Val Glu	Ile Ser	Arg Lys	Val Tyr	Lys Gly	Met Leu								
		980			985			990							
Asp Leu	Leu Lys	Cys Thr	Val Leu	Ser Leu	Glu Gln	Ser Tyr	Ala His								
		995			1000			1005							
Ala Gly	Leu Gly	Gly Met	Ala Ser	Ile Phe	Gly Leu	Leu Glu	Ile Ala								
		1010			1015			1020							
Gln Thr	His Tyr	Tyr Ser	Lys Glu	Pro Asp	Lys Arg	Lys Arg	Ser Pro								
1025			1030		1035			1040							
Thr Glu	Ser Val	Asn Thr	Pro Val	Gly Lys	Asp Pro	Gly Leu	Ala Gly								
		1045			1050			1055							
Arg Gly	Asp Pro	Lys Ala	Met Ala	Gln Leu	Arg Val	Pro Gln	Leu Gly								
		1060			1065			1070							
Pro Arg	Ala Pro	Ser Ala	Thr Gly	Lys Gly	Pro Lys	Glu Leu	Asp Thr								
		1075			1080			1085							
Arg Ser	Leu Lys	Glu Glu	Asn Phe	Ile Ala	Ser Ile	Gly Pro	Glu Val								
		1090			1095			1100							
Ile Lys	Pro Val	Phe Asp	Leu Gly	Glu Thr	Glu Glu	Lys Lys	Ser Gln								
1105			1110		1115			1120							
Ile Ser	Ala Asp	Ser Gly	Val Ser	Leu Thr	Ser Ser	Ser Gln	Arg Thr								
		1125			1130			1135							
Asp Gln	Asp Ser	Val Ile	Gly Val	Ser Pro	Ala Val	Met Ile	Arg Ser								
		1140			1145			1150							
Ser Ser	Gln Asp	Ser Glu	Val Ser	Thr Val	Val Ser	Asn Ser	Ser Gly								
		1155			1160			1165							
Glu Thr	Leu Gly	Ala Asp	Ser Asp	Leu Ser	Ser Asn	Ala Gly	Asp Gly								
		1170			1175			1180							
Pro Gly	Gly Glu	Gly Ser	Val His	Leu Ala	Ser Ser	Arg Gly	Thr Leu								
1185			1190		1195			1200							
Ser Asp	Ser Glu	Ile Glu	Thr Asn	Ser Ala	Thr Ser	Thr Ile	Phe Gly								
		1205			1210			1215							
Lys Ala	His Ser	Leu Lys	Pro Ser	Ile Lys	Glu Lys	Leu Ala	Gly Ser								
		1220			1225			1230							

Pro Ile Arg Thr Ser Glu Asp Val Ser Gln Arg Val Tyr Leu Tyr Glu
 1235 1240 1245
 Gly Leu Leu Gly Lys Glu Arg Ser Thr Leu Trp Asp Gln Met Gln Phe
 1250 1255 1260
 Trp Glu Asp Ala Phe Leu Asp Ala Val Met Leu Glu Arg Glu Gly Met
 1265 1270 1275 1280
 Gly Met Asp Gln Gly Pro Gln Glu Met Ile Asp Arg Tyr Leu Ser Leu
 1285 1290 1295
 Gly Glu His Asp Arg Lys Arg Leu Glu Asp Asp Glu Asp Arg Leu Leu
 1300 1305 1310
 Ala Thr Leu Leu His Asn Leu Ile Ser Tyr Met Leu Leu Met Lys Val
 1315 1320 1325
 Asn Lys Asn Asp Ile Arg Lys Lys Val Arg Arg Leu Met Gly Lys Ser
 1330 1335 1340
 His Ile Gly Leu Val Tyr Ser Gln Gln Ile Asn Glu Val Leu Asp Gln
 1345 1350 1355 1360
 Leu Ala Asn Leu Asn Gly Arg Asp Leu Ser Ile Trp Ser Ser Gly Ser
 1365 1370 1375
 Arg His Met Lys Lys Gln Thr Phe Val Val His Ala Gly Thr Asp Thr
 1380 1385 1390
 Asn Gly Asp Ile Phe Phe Met Glu Val Cys Asp Asp Cys Val Val Leu
 1395 1400 1405
 Arg Ser Asn Ile Gly Thr Val Tyr Glu Arg Trp Trp Tyr Glu Lys Leu
 1410 1415 1420
 Ile Asn Met Thr Tyr Cys Pro Lys Thr Lys Val Leu Cys Leu Trp Arg
 1425 1430 1435 1440
 Arg Asn Gly Ser Glu Thr Gln Leu Asn Lys Phe Tyr Thr Lys Lys Cys
 1445 1450 1455
 Arg Glu Leu Tyr Tyr Cys Val Lys Asp Ser Met Glu Arg Ala Ala Ala
 1460 1465 1470
 Arg Gln Gln Ser Ile Lys Pro Gly Pro Glu Leu Gly Gly Glu Phe Pro
 1475 1480 1485
 Val Gln Asp Leu Lys Thr Gly Glu Gly Gly Leu Leu Gln Val Thr Leu
 1490 1495 1500
 Glu Gly Ile Asn Leu Lys Phe Met His Asn Gln Val Phe Ile Glu Leu
 1505 1510 1515 1520
 Asn His Ile Lys Lys Cys Asn Thr Val Arg Gly Val Phe Val Leu Glu
 1525 1530 1535
 Glu Phe Val Pro Glu Ile Lys Glu Val Val Ser His Lys Tyr Lys Thr
 1540 1545 1550
 Pro Met Ala His Glu Ile Cys Tyr Ser Val Leu Cys Leu Phe Ser Tyr
 1555 1560 1565
 Val Ala Ala Val His Ser Ser Glu Glu Asp Leu Arg Thr Pro Pro Arg
 1570 1575 1580
 Pro Val Ser Ser
 1585

<210> SEQ ID NO 17

<211> LENGTH: 2473

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (14)..(2404)

<400> SEQUENCE: 17

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 Met Ala Ala Ala Pro Val Ala Ala Gly Ser Gly Ala

49

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ggc	cga	ggg	aga	cgg	tcg	gca	gcc	aca	gtg	gcg	gct	tgg	ggc	gga	tgg		97
Gly	Arg	Gly	Arg	Arg	Ser	Ala	Ala	Thr	Val	Ala	Ala	Trp	Gly	Gly	Trp		
		15					20					25					
ggc	ggc	cgg	ccg	cgg	cct	ggt	aac	att	ctg	ctg	cag	ctg	cgg	cag	ggc		145
Gly	Gly	Arg	Pro	Arg	Pro	Gly	Asn	Ile	Leu	Leu	Gln	Leu	Arg	Gln	Gly		
	30					35					40						
cag	ctg	acc	ggc	cgg	ggc	ctg	gtc	cgg	gcg	gtg	cag	ttc	act	gag	act		193
Gln	Leu	Thr	Gly	Arg	Gly	Leu	Val	Arg	Ala	Val	Gln	Phe	Thr	Glu	Thr		
	45				50					55				60			
ttt	ttg	acg	gag	agg	gac	aaa	caa	tcc	aag	tgg	agt	gga	att	cct	cag		241
Phe	Leu	Thr	Glu	Arg	Asp	Lys	Gln	Ser	Lys	Trp	Ser	Gly	Ile	Pro	Gln		
				65					70					75			
ctg	ctc	ctc	aag	ctg	cac	acc	acc	agc	cac	ctc	cac	agt	gac	ttt	gtt		289
Leu	Leu	Leu	Lys	Leu	His	Thr	Thr	Ser	His	Leu	His	Ser	Asp	Phe	Val		
			80					85					90				
gag	tgt	caa	aac	atc	ctc	aag	gaa	att	tct	cct	ctt	ctc	tcc	atg	gag		337
Glu	Cys	Gln	Asn	Ile	Leu	Lys	Glu	Ile	Ser	Pro	Leu	Leu	Ser	Met	Glu		
		95				100						105					
gct	atg	gca	ttt	gtt	act	gaa	gag	agg	aaa	ctt	acc	caa	gaa	acc	act		385
Ala	Met	Ala	Phe	Val	Thr	Glu	Glu	Arg	Lys	Leu	Thr	Gln	Glu	Thr	Thr		
	110					115					120						
tat	cca	aat	act	tac	att	ttt	gac	ttg	ttt	gga	ggt	gtt	gat	ctt	ctt		433
Tyr	Pro	Asn	Thr	Tyr	Ile	Phe	Asp	Leu	Phe	Gly	Gly	Val	Asp	Leu	Leu		
	125				130					135				140			
gta	gaa	att	ctt	atg	agg	cct	acg	atc	tct	atc	cgg	gga	cag	aaa	ctg		481
Val	Glu	Ile	Leu	Met	Arg	Pro	Thr	Ile	Ser	Ile	Arg	Gly	Gln	Lys	Leu		
				145				150					155				
aaa	ata	agt	gat	gaa	atg	tcc	aag	gac	tgc	ttg	agt	atc	ctg	tat	aat		529
Lys	Ile	Ser	Asp	Glu	Met	Ser	Lys	Asp	Cys	Leu	Ser	Ile	Leu	Tyr	Asn		
			160					165					170				
acc	tgt	gtc	tgt	aca	gag	gga	gtt	aca	aag	cgt	ttg	gca	gaa	aag	aat		577
Thr	Cys	Val	Cys	Thr	Glu	Gly	Val	Thr	Lys	Arg	Leu	Ala	Glu	Lys	Asn		
		175					180						185				
gac	ttt	gtg	atc	ttc	ctg	ttt	aca	ttg	atg	aca	agt	aag	aag	aca	ttc		625
Asp	Phe	Val	Ile	Phe	Leu	Phe	Thr	Leu	Met	Thr	Ser	Lys	Lys	Thr	Phe		
	190					195						200					
tta	caa	aca	gca	acc	ctc	att	gaa	gat	att	tta	ggt	gtt	aaa	aag	gaa		673
Leu	Gln	Thr	Ala	Thr	Leu	Ile	Glu	Asp	Ile	Leu	Gly	Val	Lys	Lys	Glu		
	205				210					215				220			
atg	atc	cga	cta	gat	gaa	gtc	ccc	aat	ctg	agt	tcc	tta	gta	tcc	aat		721
Met	Ile	Arg	Leu	Asp	Glu	Val	Pro	Asn	Leu	Ser	Ser	Leu	Val	Ser	Asn		
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ttc	gat	cag	cag	cag	ctc	gct	aat	ttc	tgc	cgg	att	ctg	gct	gtc	acc		769
Phe	Asp	Gln	Gln	Gln	Leu	Ala	Asn	Phe	Cys	Arg	Ile	Leu	Ala	Val	Thr		
				240				245					250				
att	tca	gag	atg	gat	aca	ggg	aat	gat	gac	aag	cac	acg	ctt	ctt	gcc		817
Ile	Ser	Glu	Met	Asp	Thr	Gly	Asn	Asp	Asp	Lys	His	Thr	Leu	Leu	Ala		
		255				260						265					
aaa	aat	gct	caa	cag	aag	aag	agc	ttg	agt	ttg	ggg	cct	tct	gca	gct		865
Lys	Asn	Ala	Gln	Gln	Lys	Lys	Ser	Leu	Ser	Leu	Gly	Pro	Ser	Ala	Ala		
		270				275					280						
gaa	atc	aat	caa	gcg	gcc	ctt	ctc	agc	att	cct	ggc	ttt	gtt	gag	cgg		913
Glu	Ile	Asn	Gln	Ala	Ala	Leu	Leu	Ser	Ile	Pro	Gly	Phe	Val	Glu	Arg		
	285				290					295				300			
ctt	tgc	aaa	ctg	gcg	act	cga	aag	gtg	tca	gag	tca	acg	ggc	aca	gcc		961
Leu	Cys	Lys	Leu	Ala	Thr	Arg	Lys	Val	Ser	Glu	Ser	Thr	Gly	Thr	Ala		

				305					310				315				
agc	ttc	ctt	cag	gag	ttg	gaa	gag	tgg	tac	aca	tgg	cta	gac	aat	gct		1009
Ser	Phe	Leu	Gln	Glu	Leu	Glu	Glu	Trp	Tyr	Thr	Trp	Leu	Asp	Asn	Ala		
			320					325				330					
ttg	gtg	cta	gat	gcc	ctg	atg	cga	gtg	gcc	aat	gag	gag	tca	gag	cac		1057
Leu	Val	Leu	Asp	Ala	Leu	Met	Arg	Val	Ala	Asn	Glu	Glu	Ser	Glu	His		
		335					340				345						
aat	caa	gcc	tcc	att	gtg	ttc	cct	cct	cca	ggg	gct	tct	gag	gag	aat		1105
Asn	Gln	Ala	Ser	Ile	Val	Phe	Pro	Pro	Pro	Gly	Ala	Ser	Glu	Glu	Asn		
	350					355			360								
ggc	ctg	cct	cac	acg	tca	gcc	aga	acc	cag	ctg	ccc	cag	tca	atg	aag		1153
Gly	Leu	Pro	His	Thr	Ser	Ala	Arg	Thr	Gln	Leu	Pro	Gln	Ser	Met	Lys		
365					370				375					380			
att	atg	cat	gag	atc	atg	tac	aaa	ctg	gaa	gtg	ctc	tat	gtc	ctc	tgc		1201
Ile	Met	His	Glu	Ile	Met	Tyr	Lys	Leu	Glu	Val	Leu	Tyr	Val	Leu	Cys		
			385					390				395					
gtg	ctg	ctg	atg	ggg	cgt	cag	cga	aac	cag	gtt	cac	aga	atg	att	gca		1249
Val	Leu	Leu	Met	Gly	Arg	Gln	Arg	Asn	Gln	Val	His	Arg	Met	Ile	Ala		
		400					405				410						
gag	ttc	aag	ctg	atc	cct	gga	ctt	aat	aat	ttg	ttt	gac	aaa	ctg	att		1297
Glu	Phe	Lys	Leu	Ile	Pro	Gly	Leu	Asn	Asn	Leu	Phe	Asp	Lys	Leu	Ile		
	415					420					425						
tgg	agg	aag	cat	tca	gca	tct	gcc	ctt	gtc	ctc	cat	ggt	cac	aac	cag		1345
Trp	Arg	Lys	His	Ser	Ala	Ser	Ala	Leu	Val	Leu	His	Gly	His	Asn	Gln		
	430				435				440								
aac	tgt	gac	tgt	agc	ccg	gac	atc	acc	ttg	aag	ata	cag	ttt	ttg	agg		1393
Asn	Cys	Asp	Cys	Ser	Pro	Asp	Ile	Thr	Leu	Lys	Ile	Gln	Phe	Leu	Arg		
445				450					455					460			
ctt	ctt	cag	agc	ttc	agt	gac	cac	cac	gag	aac	aag	tac	ttg	tta	ctc		1441
Leu	Leu	Gln	Ser	Phe	Ser	Asp	His	His	Glu	Asn	Lys	Tyr	Leu	Leu	Leu		
		465						470				475					
aac	aac	cag	gag	ctg	aat	gaa	ctc	agt	gcc	atc	tct	ctc	aag	gcc	aac		1489
Asn	Asn	Gln	Glu	Leu	Asn	Glu	Leu	Ser	Ala	Ile	Ser	Leu	Lys	Ala	Asn		
		480					485					490					
atc	cct	gag	gtg	gaa	gct	gtc	ctc	aac	acc	gac	agg	agt	ttg	gtg	tgt		1537
Ile	Pro	Glu	Val	Glu	Ala	Val	Leu	Asn	Thr	Asp	Arg	Ser	Leu	Val	Cys		
	495					500					505						
gat	ggg	aag	agg	ggc	tta	tta	act	cgt	ctg	ctg	cag	gtc	atg	aag	aag		1585
Asp	Gly	Lys	Arg	Gly	Leu	Leu	Thr	Arg	Leu	Leu	Gln	Val	Met	Lys	Lys		
	510			515				520									
gag	cca	gca	gag	tcg	tct	ttc	agg	ttt	tgg	caa	gct	cgg	gct	gtg	gag		1633
Glu	Pro	Ala	Glu	Ser	Ser	Phe	Arg	Phe	Trp	Gln	Ala	Arg	Ala	Val	Glu		
525				530				535					540				
agt	ttc	ctc	cga	ggg	acc	acc	tcc	tat	gca	gac	cag	atg	ttc	ctg	ctg		1681
Ser	Phe	Leu	Arg	Gly	Thr	Thr	Ser	Tyr	Ala	Asp	Gln	Met	Phe	Leu	Leu		
		545						550			555						
aag	cga	ggc	ctc	ttg	gag	cac	atc	ctt	tac	tgc	att	gtg	gac	agc	gag		1729
Lys	Arg	Gly	Leu	Leu	Glu	His	Ile	Leu	Tyr	Cys	Ile	Val	Asp	Ser	Glu		
	560					565					570						
tgt	aag	tca	agg	gat	gtg	ctc	cag	agt	tac	ttt	gac	ctc	ctg	ggg	gag		1777
Cys	Lys	Ser	Arg	Asp	Val	Leu	Gln	Ser	Tyr	Phe	Asp	Leu	Leu	Gly	Glu		
	575					580					585						
ctg	atg	aag	ttc	aac	gtt	gat	gca	ttc	aag	aga	ttc	aat	aaa	aat	atc		1825
Leu	Met	Lys	Phe	Asn	Val	Asp	Ala	Phe	Lys	Arg	Phe	Asn	Lys	Asn	Ile		
	590					595					600						
aac	acc	gat	gca	aag	ttc	cag	gta	ttc	ctg	aag	cag	atc	aac	agc	tcc		1873
Asn	Thr	Asp	Ala	Lys	Phe	Gln	Val	Phe	Leu	Lys	Gln	Ile	Asn	Ser	Ser		

605	610	615	620	
ctg gtg gac tcc aac atg ctg gtg cgc tgt gtc act ctg tcc ctg gac				1921
Leu Val Asp Ser Asn Met Leu Val Arg Cys Val Thr Leu Ser Leu Asp				
	625	630	635	
cga ttt gaa aac cag gtg gat atg aaa gtt gcc gag gta ctg tct gaa				1969
Arg Phe Glu Asn Gln Val Asp Met Lys Val Ala Glu Val Leu Ser Glu				
	640	645	650	
tgc cgc ctg ctc gcc tac ata tcc cag gtg ccc acg cag atg tcc ttc				2017
Cys Arg Leu Leu Ala Tyr Ile Ser Gln Val Pro Thr Gln Met Ser Phe				
	655	660	665	
ctc ttc cgc ctc atc aac atc atc cac gtg cag acg ctg acc cag gag				2065
Leu Phe Arg Leu Ile Asn Ile Ile His Val Gln Thr Leu Thr Gln Glu				
	670	675	680	
aac gtc agc tgc ctc aac acc agc ctg gtg atc ctg atg ctg gcc cga				2113
Asn Val Ser Cys Leu Asn Thr Ser Leu Val Ile Leu Met Leu Ala Arg				
685	690	695	700	
cgg aaa gag cgg ctg ccc ctg tac ctg cgg ctg ctg cag cgg atg gag				2161
Arg Lys Glu Arg Leu Pro Leu Tyr Leu Arg Leu Leu Gln Arg Met Glu				
	705	710	715	
cac agc aag aag tac ccc ggc ttc ctg ctc aac aac ttc cac aac ctg				2209
His Ser Lys Lys Tyr Pro Gly Phe Leu Leu Asn Asn Phe His Asn Leu				
	720	725	730	
ctg cgc ttc tgg cag cag cac tac ctg cac aag gac aag gac agc acc				2257
Leu Arg Phe Trp Gln Gln His Tyr Leu His Lys Asp Lys Asp Ser Thr				
	735	740	745	
tgc cta gag aac agc tcc tgc atc agc ttc tca tac tgg aag gag aca				2305
Cys Leu Glu Asn Ser Ser Cys Ile Ser Phe Ser Tyr Trp Lys Glu Thr				
	750	755	760	
gtg tcc atc ctg ttg aac ccg gac cgg cag tca ccc tct gct ctc gtt				2353
Val Ser Ile Leu Leu Asn Pro Asp Arg Gln Ser Pro Ser Ala Leu Val				
	765	770	775	780
agc tac att gag gag ccc tac atg gac ata gac agg gac ttc act gag				2401
Ser Tyr Ile Glu Glu Pro Tyr Met Asp Ile Asp Arg Asp Phe Thr Glu				
	785	790	795	
gag tgaccttggg ccaggcctcg ggaggctgct gggccagtgt ggggtgagcgt				2454
Glu				
gggtacgatg ccacacgcc				2473

<210> SEQ ID NO 18

<211> LENGTH: 797

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

Met	Ala	Ala	Ala	Pro	Val	Ala	Ala	Gly	Ser	Gly	Ala	Gly	Arg	Gly	Arg
1				5				10					15		
Arg	Ser	Ala	Ala	Thr	Val	Ala	Ala	Trp	Gly	Gly	Trp	Gly	Gly	Arg	Pro
		20						25					30		
Arg	Pro	Gly	Asn	Ile	Leu	Leu	Gln	Leu	Arg	Gln	Gly	Gln	Leu	Thr	Gly
		35					40					45			
Arg	Gly	Leu	Val	Arg	Ala	Val	Gln	Phe	Thr	Glu	Thr	Phe	Leu	Thr	Glu
	50					55				60					
Arg	Asp	Lys	Gln	Ser	Lys	Trp	Ser	Gly	Ile	Pro	Gln	Leu	Leu	Leu	Lys
65				70				75							80
Leu	His	Thr	Thr	Ser	His	Leu	His	Ser	Asp	Phe	Val	Glu	Cys	Gln	Asn
			85					90						95	
Ile	Leu	Lys	Glu	Ile	Ser	Pro	Leu	Leu	Ser	Met	Glu	Ala	Met	Ala	Phe
		100						105						110	

Val	Thr	Glu	Glu	Arg	Lys	Leu	Thr	Gln	Glu	Thr	Thr	Tyr	Pro	Asn	Thr	
		115					120					125				
Tyr	Ile	Phe	Asp	Leu	Phe	Gly	Gly	Val	Asp	Leu	Leu	Val	Glu	Ile	Leu	
	130					135					140					
Met	Arg	Pro	Thr	Ile	Ser	Ile	Arg	Gly	Gln	Lys	Leu	Lys	Ile	Ser	Asp	
145					150					155					160	
Glu	Met	Ser	Lys	Asp	Cys	Leu	Ser	Ile	Leu	Tyr	Asn	Thr	Cys	Val	Cys	
				165						170					175	
Thr	Glu	Gly	Val	Thr	Lys	Arg	Leu	Ala	Glu	Lys	Asn	Asp	Phe	Val	Ile	
			180					185						190		
Phe	Leu	Phe	Thr	Leu	Met	Thr	Ser	Lys	Lys	Thr	Phe	Leu	Gln	Thr	Ala	
	195						200					205				
Thr	Leu	Ile	Glu	Asp	Ile	Leu	Gly	Val	Lys	Lys	Glu	Met	Ile	Arg	Leu	
	210					215						220				
Asp	Glu	Val	Pro	Asn	Leu	Ser	Ser	Leu	Val	Ser	Asn	Phe	Asp	Gln	Gln	
225					230					235					240	
Gln	Leu	Ala	Asn	Phe	Cys	Arg	Ile	Leu	Ala	Val	Thr	Ile	Ser	Glu	Met	
				245						250					255	
Asp	Thr	Gly	Asn	Asp	Asp	Lys	His	Thr	Leu	Leu	Ala	Lys	Asn	Ala	Gln	
			260					265						270		
Gln	Lys	Lys	Ser	Leu	Ser	Leu	Gly	Pro	Ser	Ala	Ala	Glu	Ile	Asn	Gln	
	275						280						285			
Ala	Ala	Leu	Leu	Ser	Ile	Pro	Gly	Phe	Val	Glu	Arg	Leu	Cys	Lys	Leu	
	290					295					300					
Ala	Thr	Arg	Lys	Val	Ser	Glu	Ser	Thr	Gly	Thr	Ala	Ser	Phe	Leu	Gln	
305					310					315					320	
Glu	Leu	Glu	Glu	Trp	Tyr	Thr	Trp	Leu	Asp	Asn	Ala	Leu	Val	Leu	Asp	
				325					330						335	
Ala	Leu	Met	Arg	Val	Ala	Asn	Glu	Glu	Ser	Glu	His	Asn	Gln	Ala	Ser	
		340						345					350			
Ile	Val	Phe	Pro	Pro	Pro	Gly	Ala	Ser	Glu	Glu	Asn	Gly	Leu	Pro	His	
	355						360					365				
Thr	Ser	Ala	Arg	Thr	Gln	Leu	Pro	Gln	Ser	Met	Lys	Ile	Met	His	Glu	
	370					375						380				
Ile	Met	Tyr	Lys	Leu	Glu	Val	Leu	Tyr	Val	Leu	Cys	Val	Leu	Leu	Met	
385					390					395					400	
Gly	Arg	Gln	Arg	Asn	Gln	Val	His	Arg	Met	Ile	Ala	Glu	Phe	Lys	Leu	
				405					410						415	
Ile	Pro	Gly	Leu	Asn	Asn	Leu	Phe	Asp	Lys	Leu	Ile	Trp	Arg	Lys	His	
		420						425					430			
Ser	Ala	Ser	Ala	Leu	Val	Leu	His	Gly	His	Asn	Gln	Asn	Cys	Asp	Cys	
	435						440					445				
Ser	Pro	Asp	Ile	Thr	Leu	Lys	Ile	Gln	Phe	Leu	Arg	Leu	Leu	Gln	Ser	
	450					455					460					
Phe	Ser	Asp	His	His	Glu	Asn	Lys	Tyr	Leu	Leu	Leu	Asn	Asn	Gln	Glu	
465					470					475					480	
Leu	Asn	Glu	Leu	Ser	Ala	Ile	Ser	Leu	Lys	Ala	Asn	Ile	Pro	Glu	Val	
				485						490					495	
Glu	Ala	Val	Leu	Asn	Thr	Asp	Arg	Ser	Leu	Val	Cys	Asp	Gly	Lys	Arg	
		500						505					510			
Gly	Leu	Leu	Thr	Arg	Leu	Leu	Gln	Val	Met	Lys	Lys	Glu	Pro	Ala	Glu	
	515						520						525			
Ser	Ser	Phe	Arg	Phe	Trp	Gln	Ala	Arg	Ala	Val	Glu	Ser	Phe	Leu	Arg	
	530					535					540					
Gly	Thr	Thr	Ser	Tyr	Ala	Asp	Gln	Met	Phe	Leu	Leu	Lys	Arg	Gly	Leu	
545					550					555					560	
Leu	Glu	His	Ile	Leu	Tyr	Cys	Ile	Val	Asp	Ser	Glu	Cys	Lys	Ser	Arg	

